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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Jul 16 17:08:47 1999; MasPar time 47.89 Seconds
958.834 Million cell updates/sec

Tabular output not generated.

Title: >US-08-908-453-1 (1-1146) from US08908453.pep 8617

Description: Perfect Score: Sequence: 1 MHVNILHPQLQTMVEQWQMR.....AFNGSWSTKTNWLFHAVKHY 1146

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 55.588; Variance 118.398; scale 0.470

SUMMARIES

																							Result
į	? ? V) <u> </u>	20	19	8	17	16	Ģ	14	13	12	1	0	þ	α	7	σ	, U	4	. w	N	<u>_</u>	ult
,	167	184	188	192	198	209	215	216	226	227	253	253	259	384	456	599	621	925	1011	1151	1151	8301	Score
		·				2.4	2.5	2.5	2.6	2.6	2.9	2.9	з. 0	4.5	5.3	7.0	7.2	10.7	11.7		13.4	96.3	Query Match
	2700	4096	131	131	131	1900	1066	828	1466	854	887	133	875	816	664	1506	1634	1050	1070	1068	1068	1164	Length
) K	\ \	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2	N	2	ν	DB
04040	24000	A57099	PC4345	PC4347	PC4346	S45530	A49335	JC5706	S65741	A55404	S57219	PC4348	A36369	A59003	PC4002	JC5985	JC5500	A57134	A54600	A43322	I38110	S71792	ID
rent brocern - Yeasc		activated p	phosphoinositide 3-ki		phosphoinositide 3-ki	probable 1-phosphatid	1-phosphatidylinosito	<pre>1-phosphatidylinosito</pre>	1-phosphatidylinosito	1-phosphatidylinosito	phosphatidylinositol	phosphoinositide 3-ki	vacuolar protein-sort	phosphatidylinositol	phosphatidylinositol-		phosphoinositide 3-ki	phosphoinositide-3 ki	phosphatidylinositol	phosphatidylinositol	<pre>1-phosphatidylinosito</pre>	phosphatidylinositol-	Description
4.02e-07	3.61e-07	9.78e-10	2.55e-10	6.55e-	8.38e-12	1.83e-13	2.20e-14		4.33e-16	3.02e-16	2.23e-20	2.23e-20	2.38e-21	1.40e-42	2.13e-55	1.35e-81	1.09e-85	2.40e-143	6.47e-160	4.73e-187	4.73e-187	0.00e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	
107	109	110	114	108	110	111	110	113	108	110	112	109	109	117	140	142	140	140	145	155	1
1.2	<u>μ</u> ω	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	بر س	1.3	1.3	1.3	1.4	1.6	1.6	1.6	1.6	1.7	1.8	1
600	2829	2329	815	675	650	.647	524	513	434	350	313	312	302	301	4128	2470	1708	930	2473	2549	1
N	N	N	ω	N	N	N	N	ນ	N	N	N	N	N	N	N	N	N	2	2	N	1
S26383	A42771	S44625	T00264	B71975	D71021	C69102	A29677	S50327	G70422	A71984	S51724	C55578	A64077	A70335	JC6306	S57085	A43100	G02083	S38040	S45340	
DNA ligase (ATP) (EC	reticulocyte-binding	C50C3.6 protein - Cae	high carbon dioxide r	methyl-accepting chem	hypothetical protein	DNA mismatch recognit	complement C9 precurs	cytochrome-c oxidase	tryptophan synthase b	hypothetical protein	NSP3 protein - human	hypothetical protein	 lipopolysaccharide bi 	hypothetical protein	protein kinase (EC 2.	1-phosphatidylinosito	ataxia telangiectasia	DNA-PK - human (fragm	TOR2 protein - yeast	FKBP-rapamycin-associ	C
8.35e+00	5.11e+00	3.99e+00	1.45e+00	6.54e+00	3.99e+00	3.11e+00	3.99e+00	1.87e+00	6.54e+00	3.99e+00	2.42e+00	5.11e+00	5.11e+00	6.68e-01	1.10e-03	6.07e-04	1.10e-03	1.10e-03	2.48e-04	1.17e-05	4 . 4 . 4 .

360	Db 301 VKLTSYDVRLQQNIFVQLKLNFQGVRSERRLRCPGFVVRRQSLVLKDYCRRKPLYEPHYV
297	Qy 241 KMMKIQIEFNPNETPKSLLHTFLYEMRKLDVYDTDDPADEGWFL-QLAGRTTFVTNPD
300	SRTNA
240	Qy 181 KKTCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKKKAEINGVCE
240	Db 181 KKTCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKYKAAKLSYQMFWRKRKAEINGVCE
180	Qy 121 SKLELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWART
180	Db 121 SKLELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWART
120	Qy 61 FLANVRTSLEIKLSDFKHQLFELIAPMKWGTYSVKPQDYVERQLNNFGEIEVIFNDDQPL
120	Db 61 FLANVRTSLEIKLSDFKHQLFELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPL
60	Qy 1 MHVNILHPQLQTMVEQWQMRERPSLETENGKGSLLLENEGVADIITMCPFGEVISVVFPW
60	
ps 7;	Query Match 96.3%; Score 8301; DB 2; Length 1164; Best Local Similarity 97.2%; Pred. No. 0.00e+00; Matches 1131; Conservative 8; Mismatches 7; Indels 18; Gaps
2	ferenc #leng
	<pre>##molecule_type mRNA ##residues 1-1164 ##label MOR</pre>
	##status preliminary; nucleic acid sequence not shown
	erences MUID:96320556
lating .	A phosphatidylinositol-3-OH kinase family π
	Nature (1996) 382:536-539
	rs Morris, J.Z.;
	REFERENCE \$71792
,	13-Mar-1998
ae e	DATE
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19	TITLE phosphatidylinositol-3-OH kinase AGE-1 - Caenorhabditis
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RESULT
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Volinia, S.; Hiles, I.; Ormondroyd, E.; Nizetic, Antonacci, R.; Rocchi, M.; Waterfield, M.D. Genomics (1994) 24:472-477
Molecular cloning, cDNA sequence, and chromosomal localization of the human phosphatidylinositol pl10 alpha (PIK3CA) gene.
                                                                      138110 #type complete
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) -
#formal_name Homo sapiens #common_name man
16-Feb-1996 #sequence_revision 16-Feb-1996 #text_
21-Nov-1997
                                                               I38110; S44127
                                                                              #text_change
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##cross-references GDB:370915; OMIM:171834
#map_position 3926.3-3926.3
CLASSIFICATION #superfamily phosphatidylinosit
KEYWORDS phosphotransferase
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#accession I38110
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##molecule_type mRNA
##residues 1-1068 ##label
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ALNLWPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWFSSVVKFPDMSVIEEHANWSVS
                                                                                                                                                                                  TQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKT
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                                                                                           KLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWNNRDLFVSLFT
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Similarity 30.7%;
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phosphotransferase
#length 1068 #molecular-weight 124411 #checksum
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211; Mismatches 267; Indels
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#accession A43322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #cross-references GB:M93252; NID:g163519; PID:g163520
                                                                                                                                                                 LLFQNNEIIFKNGDDLRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLSIGDCYGLIEVV 851
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                                                                              RNSHTIMQIQCKGG-LKGALQ-FNSHTLHQWL-K----D-KNKG--EIY-DA-A--ID-
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                                         PNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKKIDN
                                                                                                                            LHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGIIEVV
                                                                                                                                                                                                             MK-LRDELR-S-ISHKMENMDSPLDPVYKLGEMIIDKAIVLGSAKRPLMLHWKNKNPKSD
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---L---F-T--R---SCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKK 943
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Similarity 30.7%;
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Phosphatidylinositol 3-kinase: structure and expression of the 110 kd catalytic subunit.
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04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
29_Jan-1999
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phosphatidylinositol 3-kinase 110K chain - bovine
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##cross-references GDB:136233

CLASSIFICATION #superfamily phosphatidylinositol 3-kinase
SUMMARY #length 1070 #molecular-weight 122761 #checksum
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#title Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification of binding site on p85.
#cross-references MUID:94067128
#accession A54600
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DSKMKPLWLVYNNKVF-GE-D-SV-GVIFKNGDDLRQDMLTLQMLRLMDLLWKEAGLDLR
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                                                                                                            LCENEMDLIWTLRQDCREIFPQSLPKLL-LSIKWNKLEDVAQLQALLQIWPKLPP-REAL 607
                                                                                                                                                                                                                                                                                                            RVRMP-SQGQ-YTYLVKHRSTWTETLNIMGDDYESCIRDPGYKK-LQML--VKKHESGIV
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                                               TRISTLVK-GMPK-DVATMK--LRDELRSISHK--MENMDSPLDPVYKLGEMIIDKAIVL
                                                                               KTLNSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQSPLNPCVILSELYVEKCKYM
                                                                                                                                NRRIGQELFWHLRSEV-HIPA--V-SVQFG-V-IL-EAYCRGSVGHMKVLSKQVEALNKL 719 : | | | | | | | | | | | | : | : |
                                                                                                                                                                              TLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALC
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Similarity 34.1%;
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phosphatidylinositol 3-kinase 110K chain isoform
#formal_name Homo sapiens #common_name man
25_oct-1994 #sequence_revision 18-Nov-1994 #text_
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Pred. No. 6.47e-160;
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.7%; Score 925; DB 2; In Best Local Similarity 33.1%; Pred. No. 2.40e-143; Matches 216; Conservative 171; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Stoyanov, B.; Volinia, S.; Hanck, T.; Rubio, I.;
Loubtchenkov, M.; Malek, D.; Stoyanova, S.; Vanhaesebroeck,
B.; Dhand, R.; Nuernberg, B.; Gierschik, P.; Seedorf, K.;
Hsuan, J.J.; Waterfield, M.D.; Wetzker, R.
#journal Science (1995) 269:693
#title Cloning and characterization of a G protein-activated human
phosphoinositide-3 kinase.
#cross-references MUID:95350661
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p_position 3q26.3-3q26.3
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                                          CTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGH
                                                                                                                                                                   HFR-YESLKHPKAYPKLFS-SVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCN 600
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                                                                                    FSDENVRAIAVQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGH
                                                                                                                           MWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEK---WKPPSVAAALT--LLGKR
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FLFWFLRSEIAQSRHY----QQ--RFAVILEAYLRGCGTAMLHDFTQQVQVIEMLQKVTL 713
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#length 1050 #molecular-weight 120444 #checksum
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#map_position 1q32

CLASSIFICATION #superfamily HsC2 phosphatidylinositol 3-kinase;

kinase C C2 region homology; PX domain homology
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1498-1612
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                                           567
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This enzyme is involved in receptor signal transduction, in a signalling complex which mediates intracellular protein trafficking, and in the regulation of cell proliferation and
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864 -EWACLPDIYVLLKQWTHMNHQDALGLLHATFPDQEVRRMAVQWIGS-LSDAELLDYLPQ 921
                                                                               806 YEFGSLREEDQRKLKDIMQK-ESLYWLTDADKKRLWEKRYYCHSEVSSLPLVLASAP-SW 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-1634 ##label BRO 1-1634 ##label BRO 1-1634 ##cross-references GB:Y11312; NID:g2076603; PID:e311430; PID:g2076604
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                                                                                                                                                 y Match 7.2%;
Local Similarity 30.7%;
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                                      YE-SCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVW 625
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phosphoinositide 3-kinase (EC 2.7.-.-) - human
#formal_name Homo sapiens #common_name man
02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change
29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. (1997) 233:537-544
Identification and cDNA cloning of a novel mammalian C2
domain-containing phosphoinositide 3-kinase, HsC2-PI3K.
                                                                                                                                                                                                               #domain catalytic #status predicted #label CAT\
#domain C2 #status predicted #label C2D\
#domain protein kinase C C2 region homology #lat
#length 1634 #molecular-weight 184856 #checksum 11:
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                                                                                                                             Conservative
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#domain phosphoinositide,3-kinase #status
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                                                                                                                                               Score 621; DB 2; Length 1634; Pred. No. 1.09e-85;
                                                                                                                             Mismatches 208;
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#checksum 1177
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Best Local Similarity 30.2%;
                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #journal Biochem. Biophys. Res. Commun. (1998) 244:531-539
#title Cloning and charaterization of a novel class II
phosphoinositide 3-kinase containing C2 domain.
#cross-references MUID:98189216
#accession JC5985
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##residues 1-1506 ##label MIS
##residues 1-1506 ##label MIS
##cross-references DDBJ:AB008791
##experimental_source liver
##experimental_source liver
truncated form is found in lung and a certain hema topoletic of
     577
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                                             KHIAKLSQKK-SPLLLSEEKRRYLWFYRLYCNNENSSLPLVLGASP-GWDE-ETVSEMHA 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYYYDALRPQ-DTEANATTYFTRLIESSL-GSVATKLNFFIHNLAQ 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCVATYVLGICDRHNDNIMLKTTGHMFHIDFGRFLGHAQ-MFGNIKRDRAPFVFTSD 1239
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KKLQMLVKKHESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYV 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MAYVING-GDKPSSR-FHDFVDLCCQAYNLIRKHTHLFLNLLGLMLSCGIPELSDLEDL 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMN 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRISLL 745
                                                                                                                                                                                                                                                                                       #superfamily HSC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology; PX domain homology
                                                                                                                                                                                                              #domain catalytic #status predicted #label CAT #length 1506 #molecular-weight 171659 #checksum 9731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC5995 #type complete
phosphoinositide 3-kinase C2gamma - mouse
#formal_name Mus musculus #common_name house mouse
06-May-1998 #sequence_revision 29-May-1998 #text_change
                                                                                                           Conservative
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                                                                                                                                 Score 599; DB 2; Length 1506; Pred. No. 1.35e-81;
                                                                                                        Mismatches
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                                                                                                        Indels 51;
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Best Local
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                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                           ##molecule_type
                                  LLSPSFVHPKVRAYAVSRL-ETASNEELLLYLLQLVQALRYDNPISSDERFQPSPLALFL 261
                                                                      LEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALT 651
                                                                                                        LSLEEKDLIWKFRFYLTRNKKAMTKFLKSV--VWTDSSEVNQALSLLDSWTEIDIDDALE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEARKFFAGIYEEAFNGSWSTKTNWLFHAVKH 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDRHNDNIMLTKSGHMFHIDFGKFLGHAQTFGGIKRDRAPFIFTSE-MEYFITE-GGK-N 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WIRKQCGIEDEKKKSKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGI
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LIGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYE-P----
                                                                                                                                            h 5.3%;
Similarity 29.1%;
166; Conservative
                                                                                                                                                                                                                   pi-3
phosphoric monoester hydrolase
#length 664 #checksum 6458
                                                                                                                                                                                                                                                                                                                                                                               Kimura, K.; Miyake, S.; Makuuchi, M.; Morita, R. Yoshida, M.; Horinouchi, S.; Fukui, Y. Biosci. Biotechnol. Biochem. (1995) 59:678-682 Phosphatidylinositol-3 kinase in fission yeast:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC4002 #type fragment
phosphatidylinositol-3 kinase (EC 3.1.3.-)
(Schizosaccharomyces pombe) (fragment)
#formal_name Schizosaccharomyces pombe
29-Jun-1995 #sequence_revision 14-Jul-1995
                                                                                                                                                                                                                                                                                                                                 PC4002
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1-664 ##label
                                                                                                                                            Score 456; DB 2; Le
Pred. No. 2.13e-55;
134; Mismatches 201;
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#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #title A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: biological roles of putative mammalian pilo and yeast Vps34p PI 3-kinase homologs during growth and development.

#cross-references_MUID:96009592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1116 ARKFFAGIYEEAFNGSWSTKTNWLFHAVKHY 1146
                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
##residues 1-816 ##label ZHO
##residues 1-816 ##label ZHO
##cross-references GB:U23480; NID:g733529; PID:g733530
##CRTION #superfamily slime mold phosphatidylinositol 3-kinase
#Plength 816 #molecular-weight 94646 #checksum 731
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Local Similarity 29.1%;
les 151; Conservation
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                                    FILGSHFYWYLTVDSVLKSSIFCSHYKTLQELYFRQLDH-TDA-QRVNAQN-KFISRLSL 481
                                                                                DR--V-IRKFAVEKLNEQLSPVTFHLFILPLIQALKYEP-RAQ-SEVGMM--LLTRALCD
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Mol. Cell. Biol. (1995)
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##residues 1-875 ##label JOH
##cross-references EMBL:U20865; NID:g662330;
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##cross-references SGD:S0004230;
p_position 12R
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                                                                   710 LDNFVKSCAGYCVITYILGVGDRHLDNLLVTPDGHFFHADFGYILGQD-PK-PFPP--L- 764
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MKLPPQIIEAF-GG-A-ESSNYD--KFRSYCFVAYSILRRNAGLILNLFELMKTSNIPDI
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                                                 VDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKTKLGIQRDRQP 1033
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                                                                                                              3.0%;
Similarity 29.9%;
52; Conservation
                                                                                                                                                                                                                                                                                                                                                                                     The sequence
S59386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein L9672.10;
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28-Mar-1991 #sequence_revision 28-Mar-1991
06-Feb-1998
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                                                                                                               Score 259; DB 2; Le
Pred. No. 2.38e-21;
46; Mismatches 64;
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#title A human phosphatidylinositol 3-kinase complex related yeast Vps34p-Vps15p protein sorting system.
#cross-references MUID:95354652
#accession S57219
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972 ESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKTKLGIQRDR 1031
                   720 EVMDTYVKSCAGYCVITYILGVGDRHLDNLVLTKTGKLFHIDFGYILGRD-PK-PLP--- 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-133 ##label HOA

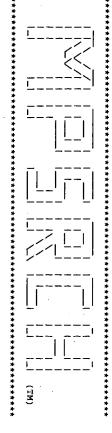
NT This enzyme plays a role in diverse cellular processes including cell migration, cell perliferation, oncogenic transformation, cell survival and intracellular trafficking of proteins.

IFICATION #superfamily phosphatidylinositol 3-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1094 STKADLDHLK-KTLFCNGESKEEARKFFAGIYEEAFNGSWSTKTNWLFHAVKHY 1146
                                                                                                                                                                                             ##molecule_type mRNA
                                                                                                                                                                                                                       ##status
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                                                                                                                                                                                 ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856 GDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVG 915
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                                                                                                     Local
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                                                                               h 2.9%;
Similarity 34.4%;
54; Conservative
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Similarity 42.0%;
34; Conservative
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phosphatidylinositol 3-kinase - human
#formal_name Homo sapiens #common_name man
27-Oct-1995  #sequence_revision 03-Nov-1995
                                                                                                                                                           #length
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#length 133 #checksum 4564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. (1997) 235:130-137 Identification of four novel human phosphoinositide 3-kinases defines a multi-isoform subfamily.
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PC4345
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phosphoinositide 3-kinase
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                                                                                                                                                           1-887 ##label VOL
jth 887 #molecula
                                                                                                                                                                                                                 preliminary
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                                                                                                                                                       #molecular-weight 100918 #checksum
                                                                             Score 253; DB 2; La
Pred. No. 2.23e-20;
32; Mismatches 60;
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Pred. No. 2.23e-20;
19; Mismatches 27;
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Panaretou, C.;
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Best Local Similarity 29.3%;
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                                      #accession $7261
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                                                                             ##residues
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                                                                                              ##molecule_type mRNA
                                                                                                                    ##status
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##residues
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##cross-references GB:L36151;
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                                                           S72615
                                                                                                                                 protein and
S65741
                                                                                                                                               Gehrmann, T.; Vereb, G.; Schmidt, M.; Klix, D.; Me Varsanyi, M.; Heilmeyer Jr., L.M.G. Biochim. Biophys. Acta (1996) 1311:53-63 Identification of a 200 kDa polypeptide as type 3 phosphatidylinositol 4-kinase from bovine brain protein and cDNA sequencing.
                                                                                                                                                                                                                                                                                                               #formal_name Bos primigenius taurus #common_name cattle 06_Dec-1996 #sequence_revision 07-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                     S65741 #type fragment
1-phosphatidylinositol 4-kinase (EC 2.7.1.67) type 3
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#length 854 #molecular-weight 96983 #checksum
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J. Biol. Chem. (1994) 269:28878-28884
Cining and characterization of a human phosphatidylinositol
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1-phosphatidylinositol 4-kinase (EC 2.7.1.67) alpha - human
#formal_name Homo sapiens #common_name man
10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change
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protein
393-414;526-531;543-559;616-636;812-829;942-955;
1098-1104;1207-1213;1277-1283;1456-1466 ##label GEW
                                                                             1-1466 ##label GEH
                                                                                                                not compared with conceptual
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Pred. No. 3.02e-16
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KEYWORDS phosphotransferase
SUMMARY #length 828 #molecular-weight 92724 #checksum 9913
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Best Local Similarity 29.3%;
Matches 46; Conservative
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Best Local Similarity 31.9%;
Matches 43; Conservative
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                                                                          1030 DROPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWNNRDLFVSLFTLML-GM 1088
  1089 ELPELSTKADLDHLK 1103
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                                   771 QLPCFHGSSTIRNLK 785
                                                                                                                  718 S--AFKLTTEFVDVM--G-GLDGDMFNY--YKMLMLQGLIAARKHMDKVVQIVEIMQQGS 770
                                                                                                                                                           971 FESVDR-FLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKTKLGIQR 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito, T.; Seki, N.; Ishii, H.; Ohira, M.; Hayashi, A.; Kozuma, S.; Hori, T.
DNA Res. (1997) 4:301-305
Complementary DNA cloning and chromosomal mapping of a novel phosphatidylinositol kinase gene.
JC5706
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1-phosphatidylinositol 4-kinase (EC 2.7.1.67) - human
#formal_name Homo sapiens #common_name man
03-Dec-1997 #sequence_revision 03-Dec-1997 #text_change
05-Jun-1998
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#length 1466 #checksum 7543
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Pred. No. 1.54e-14;
37; Mismatches 46; Indels
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Search completed: Fri Jul 16 17:09:40 1999 Job time : 53 secs.



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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Jul 16 17:06:16 1999; MasPar time 33.21 Seconds 975.343 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-908-453-1 (1-1146) from US08908453.pep

Scoring table: РАМ 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 57.005; Variance 101.644; scale 0.561

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
8617 1151 1151 1151 10115 10115 1015 105 105	Score
100 1134 1144 1144 1144 1144 1144 1144 1	Query Match
1167 1068 1068 1078 1078 1102 1104 1104 11858 1585 1585 801 814 814 814 814 814 814 814 814 814 81	Length
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AGEI_CABEL P11A_MOUSE P11A_HUMAN P11B_HUMAN P11B_HUMAN P11B_HUMAN P11B_HOMOSE P11G_PIG P11CDI P3K3_DICDI P3K3_DICDI P3K3_DICDI P3K3_DICDI P3K3_DICDI P3K4_DICDI P3K4_	ID
PHOSPHATIDYLINOSITOL	Description
3 0.00e+00 3 2.28e-223 3 5.28e-223 3 1.20e-190 3 9.62e-1182 3 91e-1182 3 3.91e-1182 3 3.24e-179 3 3.24e-179 3 3.24e-114 3 7.14e-115 4 1.2e-66 3 2.35e-37 3 3.45e-37 3 3.45e-37 3 3.45e-37 3 1.10e-25 4 1.10e-22 4 1.10e-22 4 1.10e-119 3 1.19e-116	Pred. No.

45	44	. 43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	
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1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	1.3	1.6	1.7	1.8	1.8	1.9	1.9	
827	734	697	680	662	660	600	495	334	2869	2329	1260	528	312	302	2470	2473	2549	2549	2787	2368	
μ	μ	μ	Н	۲	Н	Н	Н	-	ш	Н	هسو	۳	μ	H	ш	ш	ш	μ	Н	Н	
GYRA_HELPY	NU5C_ORYSA	AN3_XENLA	OPDA_SALTY	DDX3_MOUSE	PL10_MOUSE	DNLI_DESAM	IDH_THETH	HRCA_MYCCA	RBP1_PLAVB	YLJ6_CAEEL	YAOE_SCHPO	CO9_MOUSE	FAS3_RHOFA	LEX1_HAEIN	TOR1_YEAST	TOR2_YEAST	FRAP_HUMAN	FRAP_RAT	TEL1_YEAST	ESR1_YEAST	
DNA GYRASE SUBUNIT A (NADH-PLASTOQUINONE OXI	PUTATIVE ATP-DEPENDENT	OLIGOPEPTIDASE A (EC 3	DEAD BOX PROTEIN 3 (DE	PUTATIVE ATP-DEPENDENT	DNA LIGASE (EC 6.5.1.1	ISOCITRATE DEHYDROGENA	HEAT-INDUCIBLE TRANSCR	RETICULOCYTE BINDING P	HYPOTHETICAL 272.0 KD	HYPOTHETICAL 138.8 KD	COMPLEMENT COMPONENT C	HYPOTHETICAL 33.6 KD P	LIPOOLIGOSACCHARIDE BI	PHOSPHATIDYLINOSITOL 3	PHOSPHATIDYLINOSITOL 3	FKBP-RAPAMYCIN ASSOCIA	FKBP-RAPAMYCIN ASSOCIA	TELOMER LENGTH REGULAT	ESR1 PROTEIN.	
3.75e+00	2.15e+00	3.75e+00	2.85e+00	3.75e+00	3.75e+00	2.15e+00		2.85e+00	1.22e+00	9.19e-01		9.19e-01	1.22e+00	1.22e+00	3.33e-05	1.17e-05	3.25e-07	3.25e-07	3.77e-09	5.50e-09	

# # # # # # # # # # # # # # # # # # #	8888888	*******	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	28888		RESULT ID A
L; U56101; G1850329; SITE; PS00915; PI3_4_KINASE_1; 1. SITE; PS00916; PI3_4_KINASE_2; 1. M; PF000454; PI3_PT4_Kinase; 2. M; PF00613; PI3Ka; 1. M; PF00792; PI3K_C2; 1. M; PF00794; PI3K_rbd; 1.	uced and are n its c sage p://w	REVISIONS. REVISI	SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 96320556. MORRIS J. Z., TISSENBAUM H.A., RUVKUN G.; "A phosphatidylinositol-3-OH kinase family member regulating "A phosphatidylinositol-3-OH kinase family member."; Nafure 382:536-539(1996).	AGE-1. CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.	O-94.25; O1-NOV-1997 (REL. 35, CREATED) O1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) PHOSPHATIDYLINOSITOL 3-KINASE AGE-1 (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) (FRAGMENT).	LT 1 AGEL_CAÉEL STANDARD; PRT; 1167 AA.

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                             KSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGII
                                                             WMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLGKRCTDR
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EVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKK
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Similarity 100.0%;
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17 AA; )
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Pred. No. 0.
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PI3K/PI4K.
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               EMBL; U03279; G414995; -.

MGD; MGI:1206581; PIX3CA.

PROSITE; PS00915; PI3_4_KINASE_1; 1.

PROSITE; PS00916; PI3_4_KINASE_2; 1.

PROSITE; PS00916; PI3_4_KINASE; 7.

PFAM; PF00454; PI3_PI4_KINASE; 1.

PFAM; PF00613; PI3KA; 1.

PFAM; PF00792; PI3K_C2; 1.

PFAM; PF00792; PI3K_C2; 1.

PFAM; PF00794; PI3K_C2; 1.

PFAM; PF00794; PI3K_C3; MULTIGENE FAMII TRANSFERASE; KINASE; MULTIGENE FAMII DOMAIN

79 1053 MC1 1625 MC1 1162
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EUKARYOTA; ME
RODENTIA; SCI
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11A_MOUSE STANDARD; PRT; 1068 AA. P42337; P42337; P42337; P542337; P542337; P542337; P542347; P542347
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CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL
1-PHOSPHATE.

SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE PI3/PI4-KINASES SIMILARITY: CONTAINS 1 C2 DOMAIN.
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METAZOA; CHORDATA;
                         KINASE; MULTIGENE FAMILY.
319 428 C2 DOMAIN
799 1053 PI3K/PI4K
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AE; MURINAE;
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enzyme activity.";
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Query Match 13.5%; Best Local Similarity 31.4%; Matches 246; Conservative

Score : Pred. 1 208; M

re 1161; DB 1; L d. No. 2.53e-225; Mismatches 262;

Length

1068;

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SEQUENCE

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                                                                                    01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
(EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE (PI3K).
                                                                                                                                                                                                                                           1142
                        BOS TAURUS (BOVINE)
EUKARYOTA; METAZOA; CHORDATA; VER
ARTIODACTYLA; RUMINANTIA; PECORA;
                                                                                                                                                                     P11A_BOVIN P32871;
                                                                                                                                                                                                                                                                                                  1082
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  SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                           AVKH 1145
                                                                                                                                                                                                                                                                                                                      FSMMLGSGMPELQSFDDIAYIRKTL-ALDKTEQEALEYFTKQMNDAHHGGWTTKMDWIFH
                                                                                                                                                                                                                                                                                                                                                                KKKFGYKRERVPFVLTQDFLIVISKGAQEYTKTREFERFQEMCYKAYLAIRQHANLFINL
                                                                                                                                                                                                                                                                                                                                                                                                      DNTQAMKKYFESYDRFLYSCYGYSYATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHG
                                                                                                                                                                                                                                                                                                                                                                                                                               D----E-T--R---SCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLRDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRISTLVKGMPKDVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLGKRCTDRVIRKFAV
                                                                                                                                                                                                                                                                                                                                                   KTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWNNRDLFVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTNQRIGHFFFWHLKSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHRS-TWTET-L-NIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWRRYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REAGFSYSHTGLSNRLARDNE--LRENDKEQLRALCTRDPLSEITEQEKD-FLWSHRHYC
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                                                                                                                                                                                                                                                                                            FTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWSTKTNWLFH
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                                                                                                                                                                                  STANDARD;
AND PARTIAL SEQUENCE
                           VERTEBRATA; MAMMALIA;
ORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                  PRT;
                                                                                                                                                                                  1068
                             BOVIDAE;
                           EUTHERIA;
BOVINAE;
                           BOS
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XX MEDLINE; 92354059.

XA HILES I.D., OTSU M., VOLINIA S., FRY M.J., GOUT I., DHAND R.,

XA HILES I.D., OTSU M., VOLINIA S., FRY M.J., GOUT I., DHAND R.,

XA PANAYOTOU G., RUIZ-LARREA F., THOMPSON A., TOTTY N.F., HSUAN J.J.,

XA COUNTNEIDE S.A., PARKER P.J., WATERFIELD M.D.;

XI PANAYOTOU G., RUIZ-LARREA F., THOMPSON A., TOTTY N.F., HSUAN J.J.,

XA COUNTNEIDE S.A., PARKER P.J., WATERFIELD M.D.;

XI COUNTNEIDE S.A., PARKER P.J., WATERFIELD M.D.;

XI COUNTNEIDE S.A., PARKER P.J., WATERFIELD M.D.;

XI COUNTINOSITOL PRIDINS(4,5)P2

XI CELL 70:419-429(1992).

XI CELL 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00915; PI3_4_KINASE_1; 1.
PROSITE: PS00916; PI3_4_KINASE_2; 1.
PROSITE: PS50094; C2_DOMAIN_2: FALSE_NEG.
PFAM; PF00454; PI3_PI4_KINASE; 1.
PFAM; PF000613; PI3Ka; 1.
PFAM; PF00792; PI3K_2C2; 1.
PFAM; PF00794; PI3K_ZDd; 1.
TRANSPERASE: KINASE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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MKFLVEOMRRPDFMDALQGFLSPLNPAHQLGNLRLEECRIMSSAKRPLMLNWENPDIMSE
                                                                                                   HN---KTVS-QREGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILKQEKKDETQKVQ
                                                                                                                                                                   LNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEIARL
                                                                                                                                                                                               LEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTNQRIGHFFFWHLKSE---M
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                                                                            RDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRISTLVKGMPKDVA--T-
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799 10
1068 AA;
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larity 30.7%;
Conservative
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; Pred. No. 5.
212; Mismatcl
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PI3K/PI4K.
MW; 6916D287 CRC32;
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.28e-223;
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THE SULPH CONCRETE OF SUPERIOR SUPERIOR
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P42336; 099762;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM
(BC 2.7.1.137) (P13-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE
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                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                      STIRDIVANT S.M., AHERN J., CONROY R.R., BARNETT S.F., LEDDER L.
OLIFF A., HEIMBROOK D.C.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2
PREFERENCE FOR PTDINS(4,5)P2
-I- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL =
1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
-I- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1144
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROCCHI M., WATERRIELD M.;
"Molecular cloning, cDNA sequence, and chromosomal localization o
the human phosphatidylinositol 3-kinase pll0 alpha (PIK3CA) gene.
GENOMICS 24:472-477(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMATES;
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EUKARYOTA; METAZOA; CHORDATA;
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U79143; G1763626;
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AND PTDINS(4,5)P2
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PFAM; PF00613; PI3Ka; 1
PFAM; PF00792; PI3K_C2;
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ITE; PS00916; PI3_4_KINASE_2; 1.
ITE; PS0004; C2_DOMAIN_2; FALSE_NEG.
PF00454; PI3_PI4_KINASE; 1.
; PF00454; PI3_FI4_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIKEMYTEDLYMKDMPPSA-V-LSIRVLYGKVKLKSEEFEVGWVNMSLTDWRDELRQGQF
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                       KFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLFS 1003
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  KLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWNNRDLFVSLFT
                                                                                    TQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKT
                                                                                                        ---L---F-T--R---SCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKK
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28 C2 DOMAIN.
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PI3K/PI4K.

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H -> K (IN REF. 2).

KM -> ML (IN REF. 2).

KM -> ML (IN REF. 2).

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L -> E (IN REF. 2).

K -> E (IN REF. 2).

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Pred. No. 5.28e-223;
211; Mismatches 267;
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                                                                                                                            Query Match
Best Local :
                                                                                                                   Matches
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01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                 use by non-profit institutions us are by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HU P., MONDINO A., SKOLNIK E.Y., SCHLESSINGER J., "Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1144
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                                                                                                                                                                                                                                                                               EMBL;
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between the Swiss Institute of Biol
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                                                                                                                                                               SEQUENCE
                                                                                                                                                                                    TRANSFERASE;
                                                                                                                                                                                                                                           PROSITE; PS00915; PI3_4_KINASE_1; PROSITE; PS00916; PI3_4_KINASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIK3CB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATIDYLINOSITOL 3-KINA
(EC 2.7.1.137) (PI3-KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P42338;
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                                                                                             436
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIMATES;
  550
                         537
                                              492
                                                                     477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P85
                                                                                                                                                                                                                                                                                                                                                                                                                              1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
PATHWAY: SIGNALING PATHWAYS REGULATING CELL
SUBUNIT: HETERODIMER OF A P110 (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PHOSPHORYLATES PIDINS, PREFERENCE FOR PIDINS(4,5)P2.
                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL
                                                                                 CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPIENS
                                                                                                                                                                                                           PF00454;
PF00613;
PF00792;
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LCENEMDLIWTLRQDCREIFPQSLPKLL-LSIKWNKLEDVAQLQALLQIWPKLPP-REAL
                      RVRMP-SQGQ-YTYLVKHRSTWTETLNIMGDDYESCIRDPGYKK-LQML--VKKHESGIV
                                           HVKFPENKKQPYYYPPFDKII-EKAAEIASSDSAN-VSSRGGKKFLPVLKEILDRDPLSQ
                                                                  FEVGWVNMSLTDWRDELRQGQFLFHLWAPEPTANRSRIGENGARIGTNAAVTIEISSYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWSTKTNWLFHAV
                                                                                                                                                                                                 PF00794;
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                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   £NS (HUMĀN).
;; METAZOA; CHORDATA; VERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL. 13:7677-7688(1993).
                                                                                                                                                              1070
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(REL. 32, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
'LINOSITOL 3-KINASE CATALYTIC SUBUNIT,
'TYNASE PI10 SUBUNIT BETA) (P
                                                                                                                                                                                   4; PI3K_rbd;
KINASE; MUL1
                                                                                                                  Conservative
                                                                                                                                                                                                                                 PI3_PI4_
                                                                                                                                                                                                           PI3K_C2; 1.
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                                                                                                                           11.7%;
34.1%;
                                                                                                                                                                                 MULTIGENE FAMILY
                                                                                                                                                             122762 MW;
                                                                                                                                                                                                                                 _kinase;
                                                                                                                  170;
                                                                                                                           Score 1011;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                            of Bioinformatics
                                                                                                                                                                         PI3K/PI4K
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                                                                                                               Mismatches
                                                                                                                                                              89AA20DF CRC32;
                                                                                                                        1011; DB 1;
No. 1.20e-190;
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         002697;
15-JUL-1998 (REL. 36, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDA
15-DEC-1998 (REL. 37, LAST ANNOTATION UP
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC
(EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                   1125
                                                                                           "The G beta gamma sensitivity of a associated adaptor, pl01."; CELL 89:105-114(1997).
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STEPHENS L.R., EGUINOA A.,
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                                                                                                                                   HAWKINS P.T.;
                                                                                                                                              COADWELL
                                                                                                                                                                                    SEQUENCE FROM N.A.,
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                                                                        STEPHENS
                                                                                                                                                                            TISSUE-NEUTROPHILS;
                                                                                                                                                                                                          ARTIODACTYLA; SUIFORMES;
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                                                                     L.R.;
                                                                                                                                             J., SMRCKA A.S.,
                                                                                                                                                                                                                      METAZOA;
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                      CHORDATA;
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                                                                                                                                                                                     PARTIAL SEQUENCE
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                                                                                                                                             THELEN
                                                                                                                                          ERDJÜMENT-BROMAGE H.,
THELEN M., CADWALLADER
                                                                                                                                                                                                                                                                                                                                                                                     1068
                                                                                                                                                                                                         VERTEBRATA;
A; SUIDAE; SI
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                                                                                                                        PI3K is
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(PTDINS-3-KINASE P110)
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         CATALYTIC
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PROSITE; PS00915; PI3_4_KINASE_1; 1.

PROSITE; PS00916; PI3_4_KINASE_2; 1.

PFAM; PF00454; PI3_F14_Kinase; 1.

PFAM; PF00613; PI3K, 1.

PFAM; PF00792; PI3K, C2; 1.

PFAM; PF00792; PI3K, C2; 1.

PFAM; PF00794; PI3K, C2; 1.
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Best Local Similarity- 33.0%;
Matches 223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBI outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                            1008
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ENZYME REGULATION: WHEN BOUND TO P101 THE P13K ACTIVITY
COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYCHPIALPKHRPT-PDP-E--GDRVRAEMPNQLRKQLEAIIAT-DPLNPLTAEDKELLW
: | | | | | : : | | | : : : | | : : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLFWFLRSEIAQSRHY----QQ--RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTI 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSDENVRAIAVQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGH 693
                                          YLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDAL-TVGKSEEDAKKYFLDQIEVC
                                                                                        KYVHIDFGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEA
                                                                                                                  NLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKA 1016
                                                                                                                                                                                  SKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDG
                                                                                                                                                                                                             ----C---PIEEKF---QA-----AVERFVYSCAGYCVATFVLGIGDRHNDNIMISETG
                                                                                                                                                                                                                                                                                                                 YGCISTGDKIGMIEIVKDATTIAKIQQSTV-GNTG--AFKDEVLSHWL-K-----EK--
                                                                                                                                                                                                                                                                                                                                                                     KRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNP
                                                                                                                                                                                                                                                                                                                                                                                             KKPLWLEFKCADPTA-LSNETIGIIFKHGDDLRQDMLILQILRIMESIWETESLDLCLLP |:|| | | :|| :|| ::|| :::| | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKGMP--K-DVAT--M-KLRDELRSISH-KM-ENMDSPLDPVYKLGEMIIDKAIVLGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDELTRIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEK---WKPPSVAAALT--LLGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFR-YESLKDPKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCN 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNMSLTDWRDELRQGQFLFHLWAPEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMP 541
YEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEA
                                                                                                                                                                                                                                                                             YAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830 1075 PI3K/PI4K.
1102 AA; 126657 MW; 49DD3C11 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 981; DB 1; Le
pred. No. 9.62e-184;
178; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVITY OF
BETA-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    igh a collaboration -
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                                                                                                                                                                                     1007
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Best Local 9
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1098211; PIK3CD.

PROSITE; PS00915; PI3_4_KINASE_1; 1

PROSITE; PS00916; PI3_4_KINASE_2; 1

PFAM; PF00454; PI3_PI4_Kinase; 1.

PFAM; PF00613; PI3Ka; 1.

PFAM; PF00792; PI3K_C2; 1.

PFAM; PF00794; PI3K_C0; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-594;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT,
CEC 2.7.1.137) (PI3-KINASE P110 SUBUNIT DELTA) (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL
-!- PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
-!- PATHWAY: SICKALING PATHWAYS REGULATING CELL GROWTH.
-!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VOJTEK A.B., COOPER J.;
SUBMITTED (JAN-1997) TO
-!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIKSCU:
MUS MUSCULUS (MOUSE).
FUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
FUKARYOTA; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P11D_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U86587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC 2.7.1.137) (PI3-KINASE (PI3K) (P110DELTA).
 634
                                                                                            587
                                                                                                                         518
                                                                                                                                                          527
                                                                                                                                                                                       467
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                                                                                                                                                                                                                                                     408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                   KKKSKKADCPIAWANLMLFDYKDQLKTGERCLY-MWPSVPDEKGELLNPAGTVRGNPNTE 466
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GRALANRKIGHFLFWHLHSEM-HVPSVALR---F---GLIMEAYCRGSTHHMKVLMKQGE
                                                            VLSALELLDSSFPDCYVGSFAIKSLRKLTDDELFQ-YLLQLVQVLKYESYLDCELTKFLL
                                                                                           ESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSE-LYVMLEKWKPPS
                                                                                                                        GSGE-LYEHEKDLVWKMRHEVQEHFPEALARLL-LVTKWNKHEDVAQMLY-LLCSWPELP
                                                                                                                                                        VTIEISSYGGRVRMPSQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKH
                                                                                                                                                                                       SAAALVIYLPEV-AP-HPVY-FPALEK-I-LE-LGRHGER-GR-ITEEELQ-LREILERR 517
                                                                                                                                                                                                                      KVKLKSEEFEVGWVNMSLTDWRDELRQGQF-LFHLWAPEPTANRSRIGENGA-RIGTNAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                VAAALTILGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLL
                                                                                                                                                                                                                                                                                    230;
                                                                                                                                                                                                                                                                                                 11.3%;
Similarity 33.6%;
                                                                                                                                                                                                                                                                                                                                                775 102
1043 AA;
                                                                                                                                                                                                                                                                                                                                                                          KINASE;
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G2331238;
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                                                                                                                                                                                                                                                                                                                                                               1028
                                                                                                                                                                                                                                                                                                                                                119647 MW; 9823858E CRC32;
                                                                                                                                                                                                                                                                                                                                                                             MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSED PREDOMINANTLY IN LEUKOCYTES TO THE PI3/PI4-KINASES FAMILY.
                                                                                                                                                                                                                                                                                  Pred. No. 3.91e-
158; Mismatches
                                                                                                                                                                                                                                                                                                               Score 974;
                                                                                                                                                                                                                                                                                                                                                               PI3K/PI4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                    No. 3.91e-182
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                                                                                                                                                                                                                                                                                                                 DB 1;
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MUS.
                                                                                                                                                                                                                                                                                    233;
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                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                 1043;
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                                                                                                                                                                                                                                                                                    63;
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TRESULT OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                     WATERFIELD M.D.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5),2).
-I- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL -
1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95350661.

STOYANOV B., VOLLNIA S., HANCK T., RUBIO I., LOUBTCHENKOV M., MALEK D., STOYANOVA S., VANHAESEBROECK B., DHAND R., NUERNBERG GIERSCHIK P., SEEDORF K., HSUAN J.J., WATERFIELD M.D., WETZKE "Cloning and characterization of a G protein-activated human phosphoinositide-3 kinase.";

SCIENCE 269:690-693(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-DEC-1996 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, GAMMA ISOFORM
(EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT GAMMA) (PTDINS-3-KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11G_HU
P48736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1014
                            This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PI3K).
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                                                                                                G PROTEINS.

BATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH SUBUNIT: HETERODIMER OF A 101 KD SUBUNIT AND A 120 SUBUNIT (BY SIMILARITY).

TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIV.
SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
             European
                                                                                                                                                                                                                                                             ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAGIYEEAFNGSWSTKTNWLFHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIMIRESGQLFHIDFGHFLGNFKTKFGINRERVDFILTYDFVHVIQQGKT-N-NSEKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KATVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCTFMDSKMKPLWIMYSSEEAGSAGNV---GIIFKNGDDLRQDMLTLQMIQLMDVLWKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYDELTRISTLVK-GMPKDV-A-TMKLRDE-LRSISHK--MENMDSPLDPVYKLGEMIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKF
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4; PE00916; PI3_4_KINASE_2; 1
4; PE00454; PI3_PI4_KINASE; 1.
4; PE00613; PI3Ka; 1.
4; PE00792; PI3K_C2; 1.
4; PE00794; PI3K_C2; 1.
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC 1998 (REL. 37, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUN
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GRAY P.W., COOPER J.A., HOEKSTRA M.F.;
"pllOdelta, a novel phosphatidylinositol
that associates with p85 and is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VANHAESEBROECK B.A.M., WELHAM M.J., KOTANI K., STEIN R., WARNE ZVELEBIL M.J., HIGASHI K., VOLINIA S., DOWNWARD J., WATERFIELD "PILIOdelta, a novel phosphoinositide 3-kinase in leukocytes.", PROC. NATL. ACAD. SCI. U.S.A. 94:4330-4335(1997).
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EUKARYOTA; METAZOA; CHORDATA;
PRIMATES; CATARRHINI; HOMINIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the I
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
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PROSITE; PS00916; PI3_4_KINASE_
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HESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSE-LYVMLEKWKPP
                                                                                                                                                                             KKKSKKADCPIAWANLMLFDYKDQLKTGERCLY-MWPSVPDEKGELLNPTGT-VRSNPN- 464
                                          RGSGE-LYEHEKDLVWKLRHEVQEHFPEALARLL-LVTKWNKHEDVAQMLY-LLCSWPEL
                                                                                       TIEISSYGGRVRMPSQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQM--LVKK
                                                                                                                                T-DSAA-ALLICLPEVAPHP--V-YYPALEKILE-LGRHSE-CVHVTEEEQLQLREILER
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PF00613; PI3Ka; [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y10055; E308053; U86453; G2317894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00792; PI3K_C2; : PF00794; PI3K_rbd;
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                                                                                                                                                                                                                                                                                                                                                               253
675
1044
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE;
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253
675
                                                                                                                                                                                                                                                                                            11.1%;
                                                                                                                                                                                                                                                                                                                                                          3; MULTIGENE FAMILY.

1029 PI3K/PI4K.

253 S -> N (IN

675 R -> S (IN

119548 MW; 17E276C
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                                                                                                                                                                                                                                                                       Score 960; DB 1; Lo
Pred. No. 6.42e-179;
161; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA;
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-> S (IN REF. 2).
17E276C1 CRC32;
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                                                                                                                                                                                                                                                                                                                    Length 1044;
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P54674;
01-OCT-1996
                                                                                                                This SWI
                                                       entities
or send a
                                                                                                                                                "A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoldeum: biological roles of putative mammalian pl10 and yeasi vps34p PI 3-kinase homologs during growth and development.";
MOL. CELL. BIOL. 15:5645-5656(1995)
-i- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL - AI 1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
-i- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE 2 (EC 2.7.1.137)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1059
                                                                                                                                                                                                                                                                                        DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM
                                                                                                                                                                                                                                                                                                             (PTDINS-3-KINASE) (PI3K). PIKB OR PIK2.
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                                                                                                                                                                                                                              MEDLINE; 96009592.
ZHOU K., TAKEGAWA K.,
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                                                        s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                               S.D.,
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                                                                       //www.isb-sib
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DICTYDB; PROSITE; PROSITE;

; U23477; G733 YDB; DD01100; ITE; PS00915; ITE; PS00916;

PIKB. PI3_4_KINASE_1; PI3_4_KINASE_2;

EMBL;

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Best Local Similarity
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P3K1_DICDI ST
P54673;
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                                                                                                                   ENFKRFVTTCCSAYNILRKNTDLFINLFQLMLSTGIPELQVAEDIDYLRKAL-APGLSDE
                                                                                                                                                         DRHSDNIMITKLGHLFHIDFGHFLGNYKKKYGFKRERAPFIFTPQYMAIV-GGK--D--S
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                                                                EARKFFA
                                                                                                     HELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKE
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PF00792; PI3K_C2; 1.
PF00794; PI3K_rbd; 1
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1015
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Conservative 122;
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40 POLY-GLY.
172 POLY-SER.
226 POLY-ASN.
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Pred. No. 3.24e-154;
122; Mismatches 179;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U23476; G733520;
DICTYDB; DD01099; PIKA
PROSITE; PS00915; PI3_
PROSITE; PS00916; PI3_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoldeum: biological roles of putative mammalian pl10 and yeas: Vps34p PI 3-kinase homologs during growth and development."; MOL. CELL. BIOL. 15:5645-5656(1995).

-I- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL - AI
                                                                                                                                                                                                                                                                                                                          SEQUENCE
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ZHOU K., TAKEGAWA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE 1 (EC 2.7.1.137)
      719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-AX3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
EUKARYOTA; DICTYOSTELIUA; DICTYOSTELIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PTDINS-3-KINASE) (PI3K). PIKA OR PIK1.
                                                           659
                                                                                                             599
                                                                                                                                                                 539
                                                                                                                                                                                                                    479
                                                                                                                                                                                                                            965 IGWINVMITDFKYQLRQGMVELSLWPSDFSNPLGTCSNNPSS-SQSVGLTLEFEEFNLPV 1023
                                                                                                                                                                                                                                                                                  Local
FWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRISTLVK
                                                                                                                                                                                   LFPRKTKFSTSVSVIEQ-PPT-NI-NSN-E--MRE-FFEQITAL--DPLSD--LKQEKYN 1072
                FWYLKSD---LHDSNL-SE---RFGILLESYLYACGAHRIELLKOMEVINNLTEVAKKIK 1242
                                                    DRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRL
                                                                     NRKVREFAVTCL-EDLSEDELLDILLQLVQVLKYEPFHDSKLSRFLLRKAILNRNIGHSF 1189
                                                                                                       HVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLGKRCT
                                                                                                                                QLWTLRHY-SILFPQVLPRLM-LSVPWTQATAVDEAISLLDRWPKLKPYESLELLDAKHA 1130
                                                                                                                                                          RMPSQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQR 598
                                                                                                                                                                                                             VGWVNMSLTDWRDELRQGQFLFHLWAPEPTANRSRIGENGARIGTNAAVTIEISSYGGRV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00454; PI3_PI4_kinase;
PF00613; PI3Ka; 1.
PF00792; PI3K_C2; 1.
PF00794; PI3K_rbd; 1.
                                                                                                                                                                                                                                                                      213;
                                                                                                                                                                                                                                                                   h 9.3%;
Similarity 31.9%;
213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD01099; PIKA.
PS00915; PI3_4_KINASE_1;
PS00916; PI3_4_KINASE_2;
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59
161
294
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168
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                                                                                                                                                                                                                                                                  Score 800; DB 1; Le
Pred. No. 2.14e-142;
157; Mismatches 234;
                                                                                                                                                                                                                                                                                                                         WW;
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PI3K/PI4K
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POLY-THR.
POLY-ASN.
POLY-SER.
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POLY-ASN.
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                                                                                                                                                                                                                                                                                          Length 1570;
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                                                                                                                                                                                                                                                                   Indels
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P54675;
01-CCT-1996 (REL. 34, CREATED)
01-CCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 34, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINGSITOL 3-KINASE 3 (EC 2.7.1.137)
(PTDINS-3-KINASE) (P13K) (FRAGMENT).
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                                                                                                                                                                                                                                                 EMBL; U23478; G733524; -.
DICTYDB; DD01101; PIKC.
DICTYDB; DD0916; PI3_4_KINASE_1;
PROSITE; PS00916; PI3_4_KINASE_2;
PFAM; PF00454; PI3_PI4_Kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended Bioinformatics and the Extended Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHOU K., TAKEGAWA K., EMR S.D., FIRTEL R.A.;
"A phosphatidylinosicol (PI) Kinase gene family in Dictyostelium discoideum: biological roles of putative mammalian pil0 and yeasi vps34p PI 3-kinase homologs during growth and development.";
MOL. CELL. BIOL. 15:5645-5656(1995).

MOL. CELL. BIOL. 15:5645-5656(1995).

MOL. CELL. BIOL. 15:5645-1965(1995).

MOL. CELL. BIOL. 15:564
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EUKARYOTA; DICTYOSTELIIDA; DICTYOSTELIUM
                                                                                                               PEAM; PE00613; PI3Ka; 1.
PEAM; PE00792; PI3K_C2; 1.
PEAM; PE00794; PI3K_rbd; 1
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ZHOU K., TAKEGAWA K.,
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DOMAIN
                                                                           TRANSFERASE; KINASE; MULTIGENE FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
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POLY-ASN
                                                                                    REPEAT.
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Similarity 28.5%; Pred. No. 7.39e-131;
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P50520;
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"Schlzosaccharomyces pombe Vps34p, a phosphatidyline
"Schlzosaccharomyces pombe Vps34p, a phosphatidyline
3-kinase essential for normal cell growth and vacuol
J. CELL SCI. 108:3745-3756(1995).

-I- FUNCTION: PHOSPHATIDYLINOSITOL 3-KINASE HOMOLOG
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE VPS34 (EC 2.7.1.137)
(PTDINS-3-KINASE) (PI3K) (VACUOLAR SORTING PROTEIN
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SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
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   Matches
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01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC
(PTDINS-3-KINASE) (P13K).
                                                                                                                                                   DICTYDB;
PROSITE;
PROSITE;
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P54676;
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                      ZHOU K., TAKEGAWA K., EMR S.D., FIRTEL R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostelium
"A phosphatidylinositol roles of putative mammalian pl10 and yeast
discoideum: biological roles of putative mammalian pl10 and yeast
Vps34p PI 3-kinase homologs during growth and development.";
MOL. CELL. BIOL. 15:5645-5656(1995).

-i- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL - AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1057
                                                                                                    PFAM; PF00454; PI3_PI4_
PFAM; PF00613; PI3Ka; 1
PFAM; PF00792; PI3K_C2;
                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                          TRANSFERASE; KINASE; MULTIGENE FAMILY
DOMAIN 559 816 PI3K/PI4|
SEQUENCE 816 AA; 94647 MW; 25E09A
                                                                                                                                                                                               EMBL; U23480;
                                                                                                                                                                                                                                                                                                                                           1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
-!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96009592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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 Similarity
151; Conser
                                                                                                                                PS00916; PI3_4_KINASE_1;
PS00916; PI3_4_KINASE_2;
PS00916; PI3_4_KINASE_2;
   Conservative
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               4.5%;
29.1%;
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               Score 384; DB 1;
Pred. No. 6.58e-51
                                                          PI3K/PI4K.
25E09AF0
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) (ATVPS34).
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1065
                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A. 91:11398-11402(1994).
-!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL
1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95062775.
WELTERS P., TAKEGAWA K., EMR S.D., CHRISPEELS M.J.;
"AtVPS34, a phosphatidylinositol 3-kinase of Arabidopsis thaliana, an essential protein with homology to a calcium-dependent lipid
                                                                                                                 entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                           binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                PROSITE; PS00915; PI3_4_KINASE_1; PROSITE; PS00916; PI3_4_KINASE_2;
                                                                                    EMBL; U10669; G555700;
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SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
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              PF00454; PI3_PI4_kinase; PF00613; PI3Ka; 1.
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                                                                                                                             VITYILGIGDRHLDNLLLTDDGRLFHVDFAFILGRD-PK-PFP---PPMKLCKE-M-VEA
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                                                                                                                                                                                                                                                                                                                                                                                                                     MLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRA
  TLFCNGESKEEARKFFAGIYEEA
                                                   SGKSVDGNSHELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLK-K 1104
                                                                                                      VATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGHGKTKLGIQRDRQPFILTEHFMTVIR
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Nonara, r. Direct Submission Direct Submission Submitted (23-UUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (B-mail:ykohara@lab.nig.ac.jp,	Obara,M., Sugimoto,A., Iida,K. and NishigaKi,A. Expression map of the C.elegans genome Unpublished (1997) 2 (bases 1 to 374)	<pre>1 (sites) Kohara,Y., Motohashi,T., Tabara,H., Shin-i,T., Watanabe,H., Sano,M., Miyata,A., Ohba,T., Mitani,Y., Uesugi,H., Sugiura,I.,</pre>	Kohara unpublished coha library clone:yk355b7. Kohara unpublished coha library clone:yk355b7. Caenorhabditis elegans Eukaryotae, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis	92422932 EST; EST(expressed sequence tag). Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied	C64227 C.elegans cDNA clone yk355b7 : 5' end, single read, mRNA sequence. C64227

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                                                                                             Kohara,Y., Motohashi,T., Tabara,H., Shin-i,T., Wats
Sano,M., Miyata,A., Ohba,T., Mitani,Y., Uesugi,H.,
Obara,M., Sugimoto,A., Iida,K. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1997)
                                                                                                                                                                                                   Kohara unpublished cDNA library clone:yk260g10. Caenorhabditis elegans Eukaryotae, Metazoa; Nematoda; Secernentea; RhaRhabditina; Rhabditoidea; Rhabditidae; Peloderi
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Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied
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                                                                 Kohara,Y.
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Japan (E-mail:ykohara@lab.nig.ac.jp,
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EST; EST(expressed sequence tag).
EST; EST(expressed sequence tag).
Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:ykl92d4.
                                                                                                                                                                                                                                                                                                                                                                                                         C.elegans
C60236
                                                                 Kohara,
1111, M
                                                                                Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yu Kohara, National Institute of Genetics, Gene Network Lab; Yata
                                                                                                                                                                Sano, M., Miyata, A., Ohba, T., Mit
Obara, M., Sugimoto, A., Iida, K. a
Expression map of the C.elegans
Unpublished (1997)
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                                               1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab
Tel:+81-559-81-6854, Fax:+81-559-81-6855)
                                                                                                                                                                                                                                      Kohara,Y.,
                                                                                                                    Direct Submission
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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/tissue_type="whole animal"
61 c 94 g 86 t
/organism="Caenorhabditis elegans'
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                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:yk302a12.

Caenorhabditis elegans
Cuenorhabditis elegans
Eukaryotae; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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EST; EST(expressed sequence tag).
                                                                                                                               Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111. Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp. Tel:+81-559-81-6854, Fax:+81-559-81-6855)
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/tissue_type="whole animal"
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/db_xref="taxon:6239"
/clone="yk192d4"
               /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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/clone="yk302a12"
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C.elegans
C12541
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EST; EST(expressed sequence tag).
Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied male
                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Secernentea; Rhabditia; Rhabditida; Rhabditina;
                                                                                                                                                                                                                                                                     Sano,M., Miyata,A. and Nishigaki
Expression map of the C.elegans
Unpublished (1995)
                                                                                                                                                                 1111. Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp,
Tel:0559-81-6854, Fax:0559-81-6855)
                                                                                                                                                                                              Kohara,
                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                  Kohara, Y., Motohashi, T.,
                                                                                                                                                                                                                                                                                                                                                Secernentea; Rhabditia; Rhabditida; Rhabd
Rhabditidae; Peloderinae; Caenorhabditis.
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 74
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National Institute of Genetics, Gene Library Lab; Ye
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/sex="hermaphrodite, male"
/tissue_type="whole animal
68 c 77 g 99
                    /dev_stage="varied"
/sex="male"
                                                                                       /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/tissue_type="whole animal"
42 c 59 g 61 t
                                                                           /clone="yk152c9"
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Nishigaki,A.
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No. 2.6e-66;
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Best Local Similarity
Matches 229; Conserv
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                                                                  CTGATTGCTGGACACGGACGG----AACTCCGACGTATCTCGCAGATGCATGTTAACATTT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCCTAACCGATTGGAGAGATGAACTACGACAAGGACAATTTTTATTCCATCTGTGGGCT 1575
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                                    CTGATTGCAGGACACGGTACGGAAACTCCCGACGTATCTCGCAGATGCNTGTNANCATTT
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g2423859

EST; EST(expressed sequence tag).

Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yu

Kohara unpublished cDNA library clone:yk360d11.

Caenorhabditis elegans

Eukaryotae: Metazoa; Nematoda; Secernentea; Rhabditia; Rhal

Eukaryotae: Metazoa; Nematoda; Secernentea; Peloderinae; Caenori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohara,Y., Motohashi,T., Tabara,H., Shin-i,T., Wata
Sano,M., Miyata,A., Ohba,T., Mitani,Y., Uesugi,H.,
Obara,M., Sugimoto,A., Iida,K. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.elegans cDNA
C65154
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                                                                                                                                                                                                      /sex="hermaphrodite, male"
/tissue_type="whole animal"
55 c 60 g 56 t
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/dev_stage="varied"
                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                           /clone="yk360d11"
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95.8%;
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Pred. No. 1.8e-44;
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Pred. No. 2.4e-48;
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                                                                                             ATGGATCATGGTCTACCAAAACGAATTGGCTCTTCCACGCAGTCAAACACTACTGA 125
                                                                                                                                                                                            ATGGAGAAAGCAAAGAAGAAGCGAGAAAGTTTTTCGCTGGAATCTACGAAGAAGCCTTCA 3448
                                                                                                                                                              ATGGAGAAAGCAAAGAAGAAGCGAGAAAGTTTTTCGCTGGAATNTACGAAGAAGCCCTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sano,M., Miyata,A., Ohba,T., Mitani,Y., Uesugi,H., Sugiura, Obara,M., Sugimoto,A., Iida,K. and Nishigaki,A. Expression map of the C.elegans genome Unpublished (1997)
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Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:yk192d4.
 C10729
C.elegans
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/db_xref="taxon:6239"
/clone=""'-'
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
51 c 72 g 87 t
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cDNA clone
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yk192d4 :
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Pred. No. 4.1e-37;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3454 TCATGGTCTACCAAAACGAATTGGCTCTTCCACGCAGTCAAACACTACTGA 3504
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                                                                                                                                                                                                                                                                                                                                                                                                                     TCATGGTCTACCACAACGAATTGGCTCTTCCACGCAGTCANACACTACTGA 130
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                                                                                                                                                       EST; EST(expressed sequence tag).

Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDNA library clone:yk355b7.

Caenorhabditis elegans
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C54056
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Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied male whole animal cDNA to mRNA, clone_lib:Yuji Kohara unpublished cDN
Expression map of the C.elegans Unpublished (1997)
2 (bases 1 to 300)
                                                   Sano, M., Miyata, A., Ohba,
Obara, M., Sugimoto, A., Ii
                                                                                         Kohara, Y., Motohashi, T.,
                                                                                                                                                                                                                                                                                                                          C54056
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Tel:0559-81-6854, Fax:0559-81-6855)
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Secernentea; Rhabditia; Rhabditida; Rhabditina;
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                                                                                                                               Rhabditina; Rhabditoidea; Rhabditidae;
                                                                                                                                                 Eukaryotae; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohara,Y., Motohashi,T.,
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/db_xref="taxon:6239"
/clone="++1555"
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49 c 76 g 84 t
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/sex="male"
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98.8%;
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clone yk355b7 : 3' end,
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and Nishigaki,A.
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Pred. No. 1.4e-35;
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                                                   ., Tabara, H., Shin-i, T., Wataba, T., Mitani, Y., Uesugi, H., Iida, K. and Nishigaki, A.
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; Rhabditoidea;
                                                                                         Watanabe, H.,
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                                                                     Sugiura, I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kohara unpublished cDNA library clone:yk260g10. Caenorhabditis elegans Eukaryotae; Rhacyotae; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditoidea; Rhabditidae; Peloderi
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Location/Qualifiers
                                                                                                                                                                                                 Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. ruji Kohara, National Institute of Genetics, Gene Network Lab; Yata Kohara, National Alli, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)
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Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Y
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk355b7"
                                                                                             /organism="Caenorhabditis elegans'
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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/tissue_type="whole animal"
49 c 73 g 86 t
              /clone_lib="Yuji Kohara unpublished
/dev_stage="varied"
/sex="hermaphrodite, male"
                                                                              /clone-"yk260g10"
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/tissue_type="whole animal"
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100.0%;
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Pred. No. 6.3e-35;
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                                                                                                                                                                                                                 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Network Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:+81-559-81-6854, Fax:+81-559-81-6855)
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Kohara unpublished cDNA library clone:yk360dl1.

Caenorhabditis elegans

Eukaryotae; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Eukaryotae; Metazoa; Nematoda; Secernentea; Rhabditida;
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EST; EST(expressed sequence tag).
Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:You hermaphrodite, male whole animal cDNA to male whole animal cDNA to male whole animal cDNA to male whole animal color a
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C.elegans cDNA clone
C54778
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Obara,M., Sugimoto,A., Iida,K. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1997)
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2 (bases 1 to 300)
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                                                                                                                                                                                           AI155136 447 bp mRNA EST 30-SEP ud59f06.r1 Soares mouse uterus NMPu Mus musculus cDNA cl 5' similar to SW:P11A_MOUSE P42337 PHOSPHATIDYLINOSITOL CATALYTIC SUBUNIT, ALPHA ISOFORM ;, mRNA sequence.
AI155136
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Eukaryota; Metazoa; Chordata; Vertebrata; Rodentla; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 447)
Marra,M., Hillier,L., Allen,M., Bowles,M.,
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Utterback,T.R., Khan,M., Dubnick,M., Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCombie, W.R., Adams, M.D.,
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Rhabditina; Rhabditoidea; Rhabditidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 132; DB 10; llarity 100.0%; Pred. No. 1.3e-25; Conservative 0; Mismatches 0;
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Location/Qualifiers
1. .329
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/clone="CEMSC28"
46 c 72 g 97 t 4
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                                                   Mammalia;
Mus.
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CEMSC28.
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                                                                                                                                                                                                                                                                                                                                                                    AGCCTTCAATGGATCATGGTCTACCAAAACGAATTGGCTCTTCCACGCAGTCAAACA 3497
                                                                                                CTTCTGCAATGGAGAAAGCAAAGAAGAAGCGAGAAAGTTTTTCGCTGGAATCTACGAAGA 3440
                                                                                                                                    TGGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCATATATCCGAAAGACTCT
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                                                               GGCTTACCTAGCAATTCGGCAGCATNGCAATCTCTTCATCAACCTTTTTTCAATGATGCT
220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE_Consortium (info@image.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theising, B., Wylie, T., Lennon, G., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geisel, S., Kucaba, T., Lacy, M.,
Schellenberg, K., Steptoe, M., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: uterus; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "Clone-"1450211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DH10B"
79 c 101 g
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/sex="female"
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No. 1
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RESULT 1
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AUTHORS
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EST; EST(expressed sequence tag).
EST(EST): EST(expressed sequence tag).
Caenorhabditis elegans (strain:CB1489 him-8(e1489)) varied hermaphrodite, male whole animal cDNA to mRNA, clone_lib:Yu Kohara unpublished cDNA library clone:yk302a12.
                                                                                                                                                                                                                                                 AA174738 476 bp mRNA EST 16-FEB-1997 mt12e11.rl Soares mouse 3NbMS Mus musculus cDNA clone 620876 similar to SW:P11B_HUMAN P42338 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM; mRNA sequence.
1 (bases 1 to 476)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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C57311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohara, National Institute of Genetics, Gene Network Landli, Mishima, Shizuoka 411, Japan (E-mail:ykohara@labTel:+81-559-81-6854, Fax:+81-559-81-6855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1997) to the DDBJ/EMBL/GenBank databases. Kohara, National Institute of Genetics, Gene Network Lab; Ye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obara,M., Sugimoto,A., Iida,K. and Nisl Expression map of the C.elegans genome Unpublished (1997)
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                                                                                                                      Eukaryotae;
Vertebrata;
                                                                                                                                                        Mus musculus
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                                                                                                                                                                              house mouse.
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/sex="hermaphrodite, male"
/tissue_type="whole animal"
37 c 53 g 67 t 5 c
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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                                                                                                                  mitochondrial eukaryotes; Metazoa;
Eutheria; Rodentia; Sciurognathi;
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yk302a12 :
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Pred. No. 6.7e-10;
0; Mismatches 8;
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Rhabditidae; Peloderinae; Caenorhabditis
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,Y., Uesugi,H.,
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Muridae; N
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                                                                                                                      Murinae;
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Search completed: July 16, 1999, 19:46:31 Job time: 4755 sec
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                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%;
Best Local Similarity 64.3%;
Matches 110; Conservative
                                                                                          3100 GATTTCGGTCACATTTTGGGACACGGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAA 3159
                                                                                                                                                                                                                                                                                3040 ATCAAGGATCGTCACAGTGATAATCTGATGCTCACTGAAGATGTGGAAAATATGTCCACATT 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                           61 GATTTTGGCCACTTTCTGGGGAACTTCAAGACCAAGTTTGGAATCAACCGAGAGCGCGTC 120
                                                                                                                                                                                                                                                         High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Beritrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares mouse 3NbMS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                   Score 73.4; DB 16;
Pred. No. 1.4e-09;
0; Mismatches 61;
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Fri Jul 16 17:09:58 1999; MasPar time 46.23 Seconds 527.154 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-908-453-1 (1-1146) from US08908453.pep

Scoring table:

Sequence: 8617 1 MHVNITHPQLQTMVEQWQMR.....AFNGSWSTKTNWLFHAVKHY 1146

PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-precessing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35

34:part34 39:part39 i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 6:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part14 15:part15 16:part27 12:part27 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part20 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38

Mean 39.883; Variance 187.451; scale 0.213

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	74	Length	DB	ID	Description	Pred. No.
–	8617	100.0	1146	31	W47544	Caenorhabditis elegan	0.00e+00
N	1166	13.5	1068	Q	R46294	PtdIns 3-kinase 110 k	1.97e-89
ω	1151	13.4	1068	φ	R43341	p110.	4.35e-88
4	1151	13.4	1068	œ	R43342	Human p110.	4.35e-88
5	981	11.4		39	W90083	Porcine G-protein reg	6.76e-73
0	981	11.4		31	W23948	Porcine phosphoinosit	6.76e-73
7	. 962	11.2		ω_{ω}	W58570	Human phosphatidylino	3.33e-71
8	961	11.2		39	W90089	Human G-protein regul	4.09e-71
9	960	11.1	1044	29	W46625	Mammalian novel class	5.01e-71
10	937	10.9		31	W23947	Human phosphoinositid	5.59e-69
11	925	10.7	1049	20	W11576	Human phosphatidylino	6.52e-68
12	925	10.7		20	W11577	Human phosphatidylino	6.52e-68
13	599	7.0		29	W38756	Phosphatidyl inositol	3.42e-39
14	590	6.8		34	W70991	Human class II P13 ki	2.08e-38
15	436	5.1	1876	29	W38757	Phosphatidyl inositol	3.75e-25
16	216	2.5	817	27	W37498	Human NPIK.	4.55e-07

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	3 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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22	22	27	22	27	32	22	22	22	22	22	22	22	22	22	22	22	22	22	22	19	22	32	16	19	16	9	9	27
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ດ	ATM mutant 5319ins9.	ATM protein.	ATM mutant Leu43Pro.	-telangiectas	Ataxia-telangiectasia	t 5435del	278de1	ATM mutant 7279del6.	mutant C9140T.	mutant 2377de	mutant 6348de	mutant 9001delAG	mutant 7630del15	6	ATM mutant 4612del165	3403del17	mutant 3403del17	07de120	nt 2467de	1-like p	nt 8578de	 protein 	efi	Human RAPT1.	ä	Human PITR-f.	Human PITR-c.	Human NPIK.
.07e-	.07e-	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-	.07e-0	7	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.07e-0	.43e-0	.77e-0	.77e-0	.77e-0	.77e-0	.81e-0	.32e-	.55e-0

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Measurement of age-1 gene expression or AGE-1 protein activity can be used in the determination of the longevity of an animal. Sequence 1146 AA;	Since the agents target invertebrate diapause events, they are safer pesticides than compounds that inhibit neuro-transmission.	longevity (delay the onset of age-related conditions) in a mammal. They can be used as pesticides (against insects and nematodes).	that decrease expression or activity are used to increase	of senescence. Reduced AGE-1 mediated signalling increases longevity while complete abrogation causes developmental arrest. Agents	phosphatidylinositol-3-kinase (PI3K) involved in control	Claim 1; Fig 6; 54pp; English. The sequence is that of the AGE-1 polypeptide. AGE-1 is a	to identify modulators, potentially useful for increasing longevity	cells - and antibodies, used to determine longevity of animals and	PGF-1 TO1014.	WPI; 98-145603/13.	Morris J, Ruvkun G, Tissenbaum H;	(GEHO) GEN HOSPITAL CORP.	07-AUG-1996; US-023382	07-AUG-1997; U13914.	12-FEB-1998.	WO9805761-A1.		Region 11111116	/note= "conserved region"	ion	Key Location/Qualifiers	Caenorhabditis elegans.	Pī3K; phosphatidylinositol-3-kinase.	age-related conditions; pesticides; insects; nematodes; detection;	age-1 gene; AGE-1 polypeptide; longevity; increase; onset; delay;	Caenorhabditis elegans AGE-1 polypeptide.	03-AUG-1998 (first entry)	W47544;	W47544 standard; Protein; 1146 AA.	

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gktklgiqrdrqpfiltehfmtvirsgksvdgnshelqkfktlcveayevmwnnrdlfvs
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                                                                                                                                                             EVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKK
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                                                                         IDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHIDFGHILGH
                                                                                               idntqamkkyfesvdrflyscvgysvatyimgikdrhsdn1mltedgkyvhidfghilgh
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PN W09403609-A.

PD 17-FEB-1994.

PD 17-FEB-1994.

PD 17-FEB-1993; G01651.

PR 05-AUG-1993; GB-016554.

PR 05-AUG-1993; GB-016654.

PR 05-AUG-1992; GB-016654.

PR 05-AUG-192; GB-016654.

PR 05-AU
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PtdIns 3-kinase 110 kD catalytic subnit.
110 kD catalytic subunit; phosphatidyl inositol 3-kinase; transformation; Schizosaccharomyces pombe; nmt promoter; PtdIns 3-kinase; assay; detection; cell growth; regulation; of the standard of the stand
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R43341;
Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist; cell proliferation; inhibition; prophylaxis; therapy; platelets; neutorphil activity; 3-phosphorylated phosphoinositides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting compounds vessel plaques. Sequence 1068 AA;
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                                                                                standard;
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llarity 30.8%;
Conservative
                                                                                Protein; 1068
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Pred. No. 1.97e-89;
213; Mismatches 264;
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from a CDNA library constructed from man cDNA isolated coll line KGla. Positive clones were sequenced from the human CC roll line KGla. Positive clones were sequenced to give a human CC library constructed from man isolated from the human CC pi3 kinase pl10 sequence. This sequence has 95 percent collops with the bovine sequence. The domain encoding residues 19-cc library collection to encode the kinase which will collected a protein with pi3 kinase subunit. The gene may be used to collected protein with pi3 kinase activity, and is useful for cuseful for (ant)agonists of pi3 kinase activity which could be cuseful for stimulation or inhibition of cell proliferation and hence corpopylaxis or therapy. Platelet or neutrophil activity or blood collected salso R4342 and R46552-3.

Sequence 1068 AA.
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Best Local :
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WPI; 93-351738/44.
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Parkerpj, Volinia S,
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13-APR-1992; GB-008135.
(LUDW-) LUDWIG INST CANCER RES.
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                        rnshtimqiqckgg-lkgalq-fnshtlhqwl-k----d-knkg--eiy-da-a--id-
                                                                                      MK-LRDELR-S-ISHKMENMDSPLDPVYKLGEMIIDKAIVLGSAKRPLMLHWKNKNPKSD
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 PNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDSTKNPIEKKIDN
                                                                   LHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGIIEVV
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Similarity 30.7%;
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Best Local
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                                                                                                                                                                                                                                                                                                          a fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a cDNA library constructed from mRNA isolated from the human cell line KGla. Positive clones were sequenced to give the human PI3 kinase pi10 sequence. This sequence has 95 percent homology with the bovine sequence. The domain conty. residues 19-100 of human pi10 is sufficient to associate with the p85 kinase subunit. The protein with PI3 kinase activity is useful for screening for (ant)agonists of PI3 kinase activity which could be useful for stimulation or inhibition of cell proliferation and hence prophylaxis or therapy. Platelet or neutrophil activity or blood allocate in the passociate with proliferation and hence
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Parkerpj, Volinia S,
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Sequence 1068
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Pred. No. 4.35e-88;
211; Mismatches 267;
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15-AUG-1997;
15-AUG-1997;
27-JUN-1996;
     Nucleic acid encoding regulatory (p101) and catalytic (p120) subunits of a heterodimeric phosphatidylinositol-3' kinase in treatment and diagnosis of immune system disorders, e.g. arthritis, cancer and Alzheimer's disease Example IX; Fig 4; 75pp; English.

This sequence represents a novel catalytic subunit, p120, frophosphoinositide 3-hydroxykinase (PI3K) which is regulated by subunits of trimeric G-protein. Nucleic acid coding for p101 their fragments, are used as probes and primers for identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scroft
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W90083;
09-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                    S, Hawkins PT,
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US-916917.
US-672211.
presents a novel catalytic subunit, p120, f
3-hydroxykinase (PI3K) which is regulated
eric G-protein. Nucleic acid coding for p10
are used as probes and primers for identif
                                                                                                                                                                                                                                                                                                                       Stephens
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Porcine phosphoinositide 30H-kinase p120 subunit. 6-beta-gamma regulated phosphatidylinositol-3' kinase; phosphoinositide 30H-kinase; P13K; signal transduction; phosphatidylinositol (3,4,5)-triphosphate; G-protein; r transgenic animal; knockout animal; inflammation; arthr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p101 and p120 proteins, peptides or fusion proteins are used to treat or screen for potential agents for treating immune disorders, particularly inflammation, e.g. arthritis, septic shock, adult respiratory distress syndrome, pneumonia, asthma, allergies, reperfusion injury, atherosclerosis, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pl20 gene mutations, allelic variations or regulatory defects, particularly for the diagnosis of activation disorders (or susceptibility) in cells of the haematopoletic system. The related proteins, antibodies, agonists and antagonists can be used similarly. pl01 and pl20 proteins, peptides or fusion proteins are used to treat
                                                                                                W23948 standard;
W23948;
                                                                                   17-AUG-1998
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223; Conservative
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. No. 6.76e-73;
Mismatches 214;
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                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase, pl01 and pl20 subunits - useful for diagnosis, drug screening, clinical trial monitoring and treatment of inflammatory disorders claim 54; Fig 4; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braselmann S, Hawkins WPI; 98-077181/07.
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asthma; allergy; reperfusion injury; atheroscleros;
                                                                                                                                                                                                                                                                                                                                                         diseases.
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(ONYX-) ONYX PHARM.
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                                      MWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEK---WKPPSVAAALT--LLGKR
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fsdenvralavqklesledddvlh-yllqlvqavkfepyhdsalarfllkrglrnkrigh
                                                                       hfr-yeslkdpkaypklfs-svkwgqqeivaktyqllakrevwdqsaldvgltmqlldcn
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Similarity 33.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 weak pleckstrin homology domain, involved in membrane binding and, G-beta, gamma subunit interaction p101/120 complex."
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No. 6.76e-73;
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This is the deduced amino acid sequence of the catalytic p110 (delta subunit of human phosphatidylinostic) 3-kinase (PT 3-kinase). The sequence was deduced from a composite cDNA clone (see V58570) (closed from peripheral blood mononuclear cell and macrophage cDNA. The following are claimed: (1) a purified and isolated polynucleotide (PN) encoding p110 delta; (2) a vector comprising a CDNA as in (1); (3) a host cell stably transformed or transfected with a DNA as in (1); (4) PN encoding a lipid kinase, and hybridising to PN having the 5220 bp sequence; (5) a purified and isolated p110 delta polypeptide as in (4); (6) an antibody as in (6); and (8) a humanised antibody as in (6). p110 delta has kinase activity and may play a role in PI 3-kinase mediated
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25-NOV-1997; U21655.
25-NOV-1996; US-777405.
(ICOS-) ICOS CORP.
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sapiens.

W90089 standard; Protein; 1101 W90089; 09-MAR-1999 (first entry)

Human G-protein regulated PI3K p120 adapter subunit protein. Phosphoinositide 3-hydroxykinase; P13K; trimeric G protein; human; adapter subunit; regulatory subunit; p101, p120; catalytic subunit; adapter subunit; activation disorder; haematopoietic system; treatment; immune disorder; inflammation; arthritis; septic shock; adult respiratory distress syndrome; pneumonia; asthma; allergy; reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.

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15-AUG-1997;
15-AUG-1997;
27-JUN-1996;
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This sequence represents a novel catalytic subunit, pl20, from human phosphoinositide 3-hydroxykinase (PIJK) which is regulated by beta-gamma subunits of trimeric G-protein. Nucleic acid coding for pl01 or pl20, or their fragments, are used as probes and primers for identifying pl01 or pl20 gene mutations, allelic variations or regulatory defects, particularly for the diagnosis of activation disorders (or susceptibility) in cells of the haematopoletic system. The related proteins, antibodies, agonists and antagonists can be used similarly. The pl01 and pl10 proteins, peptides or fusion proteins are used to treat or screen for potential agents for treating immune disorders, particularly inflammation, e.g. arthritis, septic shock, adult respiratory distress syndrome, pneumonia, asthma, allergies, reperfusion injury, atherosclerosis, Alzheimer's disease and cancer.
   1016
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ylalrhhtnlliilfsmmlmtgmpqltskedieyirdal-tvgkneedakkyfldgievc
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                                                                                                  flfwflrseiagsrhy----qq--rfavileaylrgcgtamlhdftqqvqviemlqkvtl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAVLPMGEMIGIIEVVENCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKK
                                                                                                                                                                                                                                                                     kkplwlefkcadpta-lsnetigiifkhgddlrqdmlilqilrimesiwetesldlcllp
                                                                                                                                                                                                                                                                                                                         LVKGMP--K-DVAT--M-KLRDELRSISH-KM-ENMDSPLDPVYKLGEMIIDKAIVLGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVW
                                 KYVHIDFGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEA
                                                                                                                                                                                                                                                  KRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNP
                                                                                                                                                                                                                                                                                                                                                       diksisaekydvssqvisqlkqklenlqnsqlpesfrvpydpglkagalaiekckvmask
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                                                                                                                                                                                                            ygcistgdkigmieivkdattiakiqqstv-gntg--afkdevlnhwl-k-----ek--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 32.8%; 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-916917.
US-672211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 961; DB 39;
Pred. No. 4.09e-71;
176; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŗ
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1074
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                                                                                                                                                                                                                                                                                                                                                                                PT Auto-phosphorylating peptide with phosphatidyl:inositol
PT 3-kinase-like activity, designated pl10delta - useful for
Controlling cell motility, particularly of metastatic cancer cells
PS Disclosure; Fig 1h; 72pp; English.
CC The present sequence represents a novel autophosphorylating protein
CC that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and
CC is designated pl10-delta. The protein is expressed selectively in
CC white blood cells and melanomas. The protein is a lipid kinase with
CC broad phosphoinositide specificity and specific tissue localisation,
CC possibly involved in regulation of melanoma metastases (it is not
CC expressed in normal melanocytes). DNA fragments encoding the present
CC expressed in normal melanocytes). DNA fragments encoding the present
CC similar analysis can be done at the protein level using antibodies in
CC standard immunoassays. These assays are particularly used for diagnosing
CC and predicting motility/invasiveness of metastatic cancer cells. The
CC protein can be used in human or veterinary medicine for controlling
CC motility of cells, where the protein increases motility while antisense
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1996; GB-01146U.
(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                     motility of cells, where the protein increases sequences are used to reduce it. note: this record is revised to include second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998 (first entry)
22-JUN-1988 (revised entry)
22-JUN-1988 (revised entry)
Mammalian novel class I Pl3 klnase designated pl10-delta.
Autophosphorylate; Pl3; phosphatidylinosicol 3-hydroxy; k
activity; pl10-delta; melanoma; lipid kinase; metastase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1075
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W46625 standard;
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                           nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-042196/04.
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30-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoinositide specificity; regulation;
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               rgsge-lyehekdlvwklrhevqehfpealarll-lvtkwnkhedvagmly-llcswpel: || | | | ; | ; | | |
                                                                                                                            TIEISSYGGRVRMPSQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQM--LVKK
                                                                                                                                                          t-dsaa-alliclpevaphp--v-yypalekile-lgrhse-cvhvteeeglqlreiler
                                                                                                                                                                                     rdkgwtvqfnwflhlv
                                                               HESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSE-LYVMLEKWKPP
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                           sequence.
                                                                                                                                                                                                                                                             Conservative
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/note= "proline-rich
400..439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1044
                                                                                                                                                                                                                                                                          Score 960; DB 29;
Pred. No. 5.01e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                           Mismatches 229;
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                                                                                                                                                                                                                                                                                                                                                         DR
                                                                                                                                                                                                                                                                                       Length 1044;
                                                                                                                                                                                                                                                                                                                                                         line
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                                                                                                                                                                                          26-JUN-1997; U11219.
27-JUN-1996; US-672211.
(ONYX-) ONYX PHARM.
Braselmann S, Hawkins PT, S
WPI; 98-077181/07.
DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase, pl01 and p120 subunits - useful for diagnosis, drug screening, clinical trial monitoring and treatment of inflammatory disorders Claim 55; Fig 11; 151pp; English. This is the deduced amino acid sequence of the p120 catalytic subunit of human G-protein regulated phosphatidylinositol-3' kinase (P13K), a heterodimeric enzyme which produces the intracellular
                                                                                                                                                                                                                                                                     WO9749818-A2.
31-DEC-1997.
26-JUN-1997; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human phosphoinositide 30H-kinase pl20 subunit. 6-beta gamma regulated phosphatidylinositol-3' kinase; plg; phosphoinositide 30H-kinase; Pl3; signal transduction; phosphatidylinositol (3,4,5)-triphosphate; G-protein; recept transgenic animal; knockout animal; inflammation; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               septic shock; adult respiratory distress syndrome; pneumonia;
asthma; allergy; reperfusion injury; atherosclerosis; cancer;
Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage_site
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/note= "v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "cryptic thrombin 310..315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 40..41
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Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating inflammatory response disorders can be identified by screening assays using a G protein activated P13K, or a cultured host cell that expresses the p101 gene. Antagonists of G protein stimulated P13K (acting through the p101 subunit, especially by disrupting the interaction between the p101 and p120 subunits) can be used to treat arthritis, septic shock, adult respiratory distress syndrome (ARDS), pneumonia, asthma, allergies, reperfusion injury, atherosclerosis, cancer and Alzheimer's disease. The nucleic acids and their products can also be used for diagnosis, disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger phosphatidylinositol (3,4,5)-triphosphate in response to activation of trimeric G protein-linked receptors. This novel protein, which also contains a regulatory subunit, pl01 (see W23949), is found in cells of haematopoietic origin and is involved in immune system responses which cause inflammation. Human pl20 rnna was obtained from a leukocyte cDNA library. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA was obtained from a leukocyte cDNA library. The invention encompasses pig and human pl01 and pl20 uncleotides (see V04633-34), host cell expression systems, pl01 and pl20 proteins (see W23946-49) fusion proteins, polypeptides and peptides, antibodies to these proteins, and transgenic and knockout animals. Compounds which are
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CC A 402 bp cDNA fragment was amplified from a human bone marrow CC library using PCR primers corresponding to amino acid sequences CC KNGDDLR and HIDFG. The amplified fragment was used to probe a human CC U937 cell cDNA library and several overlapping clones were isolated. CC The largest clone had a sequence coding for a protein having the CC phosphatidylinositol 3-kinase (PI3K) that differs in its regulatory CC mechanism from the known PI3K-alpha and beta enzymes. The new enzyme CC has been designated PI3K-gamma and can be used as an immunogen. The CC constanting cell proliferation, receptor-mediated signal CC transmission, histamine secretion, nerve cell differentiation, glucose constants of the constant of the
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Hanck T, Stoyanov B,
WPI; 96-172545/18.
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RLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDELTRIST
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                                                                                       CTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGH
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claims"
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n as 741-745 in the
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                                                                           then isolated. The enzyme can be used as an immunogen. The enzyme antibodies against it or nucleic acid encoding it can be used for modulating cell proliferation, receptor-mediated signal transmission, histamine secretion, nerve cell differentiation, glucose transport and anti-lipolytic activity or for treating
                                                                                                                                                             library using PCR primers corresponding to amino acid sequences KNGDDLR and HIDFG. The amplified fragment was used to probe a human U937 cell cDNA library and several overlapping clones were isolated. The largest clone coded for a protein of 1049 residues. The protein is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its regulatory mechanism from the known PI3K-alpha and beta enzymes. The new enzyme has been designated PI3K-gamma. Another clone, coding for a PI3K-gamma having the present sequence of 1050 residues, was the resulted which the present sequence of 1050 residues, was the resulted which the present sequence of 1050 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human phosphatidylinositol 3-kinase PI3K-gamma. Phosphatidylinositol 3-kinase; gamma, PI3K; immunogen; immobiliferation; receptor-mediated signal transmission; histamine secretion; nerve cell differentiation; glucose temodulation; regulation; Alzheimer's disease; lipolysis.
                                                                glucose transport and anti-lipolytic Alzheimer's disease.
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Hanck T, Stoyanov
WPI; 96-172545/18.
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W11577 standard;
W11577;
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A 402 bp cDNA fragment was amplified from a human bone marrow
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04-SEP-1997;
12-FEB-1997;
29-FEB-1996;
                                                                                                                                                                                    22-JUN-1998 (first entry)
22-JUN-1998 (first entry)
Phosphatidyl inositol 3-kinase cdk-m.
Phosphatidyl inositol 3-kinase; signal transduction; cell cycle; antagonist; inflammatory joint disease; cell proliferation; canc usoriasis; restenosis; atherosclerosis; therapy; diagnosis; mous
                                                                                                                                                                                                                                                                                                                  1068
                                                                                                     Misc_difference
                                                                                                                                                                                                                                                                   W38756 standard;
                                    WO9731650-A1.
                                                                                Domain
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YEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFF
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216; Conservative
 US-609049
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941
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1590..1726
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1175..1345
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Best Local S
Matches 17
    1115
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                       eatifftrliess1-gsiatkfnffihnlag
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172; Conservative
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pred. No. 3.42e-39;
137; Mismatches 210;
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RESULT 14 ID W70991

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human class II phosphoinositide lipid (P13) kinase designated PIM3-CZalpha. It is characterised as a class II kinase due to the presence of a conserved C2 domain found in murine and Drosophila class II P13 kinases, its apparent lack of a p85 binding site and a substrate affinity to inositol lipids PtdIns and PtdIns(4)p. The protein has resistance to p13 kinase inhibitors Wortmannin and LY294002. Antibodies against the protein (optionally humanised), are used to identify class II P13 kinases. Antisense sequences, antibodies or dominant negative mutants of the p13-CZalpha protein, are useful in huma or veterinary medicine to block class II kinases. They can be used to treet tumour cells where the phenotype is associated with expression of p14-CZalpha protein.
     1365
                                                                                                                                                                                                                                                                                                                                                                                                              1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding phospho:inositol kinase 3-C2 alpha fragments - useful for, e.g. treatment of tumour cells where phenotype is associated with expression of kinase Claim 3; Fig 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-1998 (first entry)
Human class II P13 kinase-C2alpha.
Human; class II phosphoinositide l
PIK3-C2alpha; class II; resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P13-C2alpha
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28-JAN-1997; GB-001652
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19-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 klldilhk-dsslglskedkaflwekryycfkh-pnclpkilasap-nwk-wgnlaktys 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match
Focal Similarity
thes 175; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n J, Waterfield MD;
98-427960/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ellkg-tklvqllggvaekvrqasgsarqvvlqrsmervqsffqk-nkcrlplkpslvak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nsslvqfllsralgniqiahnlywllk-d-a-lhdvqf-stryehvlgallsvggkrlre 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLQMLVKKHESGIVLEEDEQRHVWMWRRYIQKQEPD-LLIVLSELAFVWTDRENFSELYV 636
aeatifftrliessl-gsiatkfnffihnlag 1395
                                                  SHELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESK
                                                                                                                                                   DRHSDNLMLTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMTVIRSGKSVDGN
                                                                                                                                                                                                                                                        IRKQCGIEDEKKKSKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIK
                                                                                                                                                                                                                                                                                                                                                                                                      iwlkegldlrmvifkclstgrdrgmvelvpasdtlrkiqveyg-vtgsfkd-kp--laew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRI - - SLLMEAYLRGNE
                                                                                                                                                                                                                                                                                                                                                          IWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMIIDKAIVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHIKIITRQVDMVDELTRISTLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLG
                                                                                               ir-fqlfvdlccqaynlirkqtnlflnllslmipsglpeltsiqdlkyvrdalqpqt-td
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a protein.
1686 AA;
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ilarity 30.6%;
Conservative
                                                                                                                                                                                                                                                                                                          np---s--e----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 590; DB 34; 1
Pred. No. 2.08e-38;
139; Mismatches 204;
                                                                                                                                                                                                                                                                                                     e---ey-e---k--as-enflyscagccvatyvlgic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                  1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  belongs to a novel class of phosphatidyl inositol 3 kinases that contain a C2 domain, are capable of phosphorylating a D3 hydroxyl of an inositol ring in phosphatidyl inositol and phosphatidyl inositol and phosphatidyl inositol and phosphatidyl inositol and phosphatidyl inositol classed that control e.g. cell cycle progression and intracellular cascades that control e.g. cell cycle progression and intracellular protein sorting. The amino acid sequence was deduced from an isolated cDNA sequence (see T80200). It shows 34% identity and 48% similarity to mouse cpk-m (see W38756). Novel phosphatidyl classed to 3 kinases can be used to screen for agonists/antagonists of activity and in a claimed method of treating a disorder caused by dysregulation of a growth factor activation signalling cascade. Antagonists may reduce Ras activation allowing treatment of proliferative disorders such as atherosclerosis, inflammatory joint disease, psoriasis, restenosis following angioplasty, and cancer.
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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W38757
W38757;
                                                                                                                                                                                                                                                                                                                              1059
                                    1288
                                                                                                                                                                                                                                                    1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein sequence comprises cpk, a Drosophila polypeptide that belongs to a novel class of phosphatidyl inositol 3-kinases that contain a C2 domain, are capable of phosphorylating a D3 hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphatidyl inositol 3-kinase cdk. Phosphatidyl inositol 3-kinase; signal antagonist; inflammatory joint disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114 EEARKFFAGIYEEAFNGSWSTKTNWLFHAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated phospatidyl inositol-3 kinase polypeptide used develop products for diagnosis and therapy, particularly for proliferative disorders, e.g. inflammatory joint diseases, or Claim 5; Fig 10; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-1996; US-609049.
(REGC ) UNIV CALIFORNIA.
Chen Y, Molz L, Williams
WPI; 97-448442/41.
                                                                                                                                                                                1176
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9731650-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis;
835
                                                                                                                                                                                                                    655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1997; U02193
                                                                                                                                                                     ahhmywll-vh-s-lpd-d--phnsigaamvdqeydesqvtqvryyrrnkmmlralmaic 1229
WKNKNPKSDLHLPFCAMIFKNGDDLRQDM-LVLQVLEVMDNIWK-AANIDCCLNPYAVLP
                                                                                                    g\text{-}ekmlqrfmyqhrmcqklttiaesvkeakesmrqkslaagmdevhqdlleqpt\text{-}clplg
                                                                                                                                          GHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRIS
                                                                                                                                                                                                                KRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRI 714
                                                                                                                                                                                                                                         EQRHY-WMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLG
                                                                                                                                                                                                                                                                                                                           errevfwekrlylqsypnalpkvlha-ahsw-dyanlidlhallhswaplsplqslelll 1116
                                                                    TLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLGEMIIDKAIVLGSAKRPLMLH
                                -pelev-tgvsvrncs-yf-nsntlplkinfvgpdaeslpaifkcgddlqqdqltiqlir
                                                                                                                                                                                                                                                                                                                                                                 ch 5.1%;
l similarity 24.9%;
l38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       psoriasis,
1876 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restenosis; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1740..1876
/note= "C2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420..434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Claim 10"
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                                                                                                                                                                                                                                                                                                                                                                 Score 436; DB 29;
Pred. No. 3.75e-25;
147; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal transduction; cell c
disease; cell proliferation;
lerosis; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1876;
                                                                                                                                                                                                                                                                                                                                                                   Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or cancer
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892
                                                                    834
                                                                                                        1287
                                                                                                                                            774
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Search completed: Fri Jul 16 17:10:53 1999 Job time: 55 secs.

* * * * *	(M)

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Jul 16 17:07:14 1999; MasPar time 67.25 Seconds 930.070 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-908-453-1 (1-1146) from US08908453.pep 8617

1 MHVNILHPQLQTMVEQWQMR.....AFNGSWSTKTNWLFHAVKHY 1146

Scoring table: PAM 150 Gap 11

Searched: 179066 segs, 54579741 residues

Post_processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_1nvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 55.192; Variance 111.319; scale 0.496

SUMMARIES

Result	Score	% Query Match	Length	DB .	ID	Description	Pred. No.
_	1170	13.6	1068	13	042391	PHOSPHOINOSITIDE 3-KIN	1.19e-201
2	1165	13.5	1083	14	039483	GAG-V-PHOSPHOINOSITIDE	1.27e-200
ω	983	11.4	1088	G	P91634	PHOSPHOINOSITIDE 3-KIN	2.24e-163
4	899	10.4	1068	4	000334	PHOSPHATIDYLINOSITOL 3	2.62e-146
v	638	7.4	1505	11	070173	PHOSPHOINOSITIDE 3-KIN	5.04e-94
o	621	7:2	1634	4	000750	PHOSPHOINOSITIDE 3-KIN	1.13e-90
7	600	7.0	1506	11	070167	PHOSPHATIDYLINOSITOL 3	1.53e-86
	599	7.0	1658	11	Q61182	PHOSPHATIDYLINOSITOL 3	2.40e-86
٠-, س	582	6.8	76	ψ	Q17482	AGE-1 PROTEIN (FRAGMEN	5.16e-83
10	590	6.8	1448	4	075747	PI3-KINASE.	1.40e-84
11	589	6.8	1509	11	Q61194	PHOSPHATIDYLINOSITOL 3	2.20e-84
12	590	6.8	1686	4	000443	PHOSPHOINOSITIDE 3-KIN	1.40e-84
13	452	5:2	1876	u	Q24453	PHOSPHOINOSITIDE 3-KIN	6.65e-58
. 14	446	5.2	1876	տ	001938	PHOSPHOINOSITIDE 3-KIN	9.18e-57
15	446	5:2	1876	u	Q24209	PHOSPHOINOSITIDE 3-KIN	9.18e-57
, 16	433	ა	1607	Ģ	Q20187	F39B1.1 PROTEIN.	2.66e-54
17	400	4.6	653	11	070168	PHOSPHATIDYLINOSITOL 3	4.25e-48
18	354	4.1	1035	10	081129	PHOSPHATIDYLINOSITOL 4	1.39e-39
. 19	337	3.9	814	10	022695	PHOSPHATIDYLINOSITOL 3	1.75e-36
. 20	317	3.7	873	ū	001424	SIMILARITY TO PHOSPHAT	7.16e-33

21 281 3.3 732 10 004269 PHOSPHATIDYLINOSITOL 3 1.73e-26 22 257 3.0 887 11 088763 PHOSPHATIDYLINOSITOL 3 2.47e-22 23 253 2.9 887 4 015134 PHOSPHATIDYLINOSITOL 3 1.19e-21 24 250 2.9 944 5 P91635 1-PHOSPHATIDYLINOSITOL 3.86e-21 25 2.3 2.7 379 10 081281 PHOSPHATIDYLINOSITOL 4.13e-18 26 2.1 1466 6 028925 TYPE 3 PHOSPHATIDYLINO 4.08e-17 27 226 2.6 2043 6 002811 PHOSPHATIDYLINOSITOL 4.13e-18 27 2.2 2.5 2.6 2043 6 002811 PHOSPHATIDYLINOSITOL 4.19le-17 28 2.1 2.5 801 6 002811 PHOSPHATIDYLINOSITOL 4.19le-17 29 214 2.5 801 6 002811 PHOSPHATIDYLINOSITOL 4.19le-17 29 214 2.5 801 6 PHOSPHATIDYLINOSITOL 4.1.29e-15 30 217 2.5 816 11 008561 PHOSPHATIDYLINOSITOL 4.1.29e-15 31 216 2.5 801 4 P78405 PHOSPHATIDYLINOSITOL 4.1.29e-15 32 214 2.5 816 11 008561 PHOSPHATIDYLINOSITOL 4.1.29e-15 33 216 2.5 828 4 015096 PHOSPHATIDYLINOSITOL 4.1.29e-15 34 204 2.4 977 3 074714 PHOSPHATIDYLINOSITOL 4.1.29e-15 35 186 2.2 2619 5 022258 PHOSPHATIDYLINOSITOL 4.1.59e-13 36 180 2.1 604 5 022057 SIMILAR TO PHOSPHATIDY 8.80e-10 37 170 2.0 4096 4 013327 DNA DEPENDENT PROTEIN 2.84e-08 38 157 1.8 2354 5 076222 PHOSPHATIDYLINOSITOL 3.28e-06 39 155 1.8 2354 5 076222 PHOSPHATIDYLINOSITOL 3.28e-06 40 147 1.7 1583 5 076222 PHOSPHATIDYLINOSITOL 3.29e-05 41 140 1.6 3056 4 093007 ATAXIA TELANGIECTASIA. 5.40e-04 44 140 1.6 4128 11 088187 DNA-DEPENDENT PROTEIN 5.40e-04 45 140 1.6 4128 11 088187 DNA-DEPENDENT PROTEIN 5.40e-04																									
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	5.40e-04	5.40e-04	5.40e-04	.5.40e-04	8.14e-05	5.92e-05	4.41e-06	2.28e-06	2.84e-08	8.80e-10	1.05e-10	1.55e-13	1.79e-15	3.78e-15	1.79e-15	1.23e-15	3.78e-15	1.91e-17	4.08e-17	6.05e-18	4.13e-18	3.86e-21	1.19e-21	2:47e-22	1.73e-26

ALIGNMENTS

Qy	뭥	Qy	밁	Qy	₽.	Ma Be	SQ	DR R	DR.	DR S	בל ק	DR.	DR	R :	3 2	R R	RA A	RX	RC	공 주 장	8	റ്റ	S	1 1	R	멸	Šŧ	RESULT
499 LFHLWA-PEPTANR-SRIGENGARIGTNAA-VTIEISSYGGRVRMPSQGQYTYLVKH 552	442 ALNIWAVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWESNPVKFPDMTVIEEHANWTIS 501	441 WIKEMTIEDLYMKDMPPSA-V-LSIRVLYGKVKLKSEEFEVGWVNMSLIDWRDELRQGQF 498	RLCLSICSVKGRKGAKEEHCPLAW	385 SIMDLDANLMIRPVNISGF-DFPA-DVD-MYVRIEFSVYVGTLTLASK-STTKVNAQFAK 440		Query Match 13.6%; Score 1170; DB 13; Length 1068; Best Local Similarity 30.6%; Pred. No. 1.19e-201; Matches 239; Conservative 213; Mismatches 266; Indels 64; Gaps 40;	SEQUENCE 1068 AA; 124287 MW; 5E791837 CRC32;	<pre>PF00794; PI3K_rbd;</pre>	PF00792;		_	PS00915; PI3_4	EMBL; AF001076; G2245506;	SCIENCE 276:1848-1850(1997).	TIANSTOLMACTOR OF CHICKER CELLS BY THE GENE ENCOUTING THE CALATYCIC	the game encoding the	CHANG H.W., AOKI M., FRUMAN D., AUGER K.R., BELLACOSA A.,	MEDLINE; 97334438.	RAIN;	SEQUENCE FROM N.A.	NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS	OTA; MET	GALLUS GALLUS (CHICKEN).		(TREMBLREL. 05,	01-JAN-1998 (TREMBLREL. 05, CREATED)	042301 FARBERSKI, FAL, 1000 FA.	1 A2301 DDET TATNABY: DDM: 1068

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PFAM;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GAG-Y-PHOSPHOINOSITIDE 3-KINASE CATALYTIC SUBUNIT F
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97334438.
                                                                                                                                                                                                                                                                                                                                                                                                                      AVIAN SARCOMA VIRUS 16. VIRUSES; RETROID VIRUSES;
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                                                     SEQUENCE
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                                                                                                     PF00794;
                                                                                                                         PF00454; PI3_PI4_kinase; PF00613; PI3Ka; 1. PF00792; PI3K_C2; 1.
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  13.5%;
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                                                  F0D9D1C3 CRC32;
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Matches 239; Conser
                                                                    P91634 PRELIMINARY; PRT; 1088 AA.

P91634;
01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHOINOSTIDE 3-KLANSE, DP110.
DROSOPHILA MELANGASTER (FRUIT FLY)
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPOI
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYI
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     SEQUENCE FROM N.A.
                                                      DROSOPHILIDAE;
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                                                                                                     TRACHEATA; HEXAPODA;
                                                                                                                                                                                     UPDATE)
                                                                                  EPHYDROIDEA;
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Best Local
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PFAM; PF00611; PI3Ka; 1.
PFAM; PF00792; PI3K_C2; 1.
PFAM; PF00794; PI3K_rbd; 1.
PFAM; PF00794; PI3K_rbd; 1.
SEQUENCE 1088 AA; 127005 MW; B20C06B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97133288.
LEEVERS S.J., WEINKOVE D., MACDOUGALL L.K., HALEN L.,
WATERFIELD M.D.;
"The Drosophila phosphoinositide 3-kinase Dp110 promotes
                    01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE DELTA CATALYTIC SUBUN
HOMO SAPIENS (HUMAN).
EUKARYOTA, METAKOA; CHORDATA; VERTEBRATA; MAMMALIA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                             1131
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  LPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKK
                                                                                                                                                                                                                                                                                                                                                                                                          L---WVVFE-NADVNASDVHIIFKNGDDLRQDMLTLQMLRVMDQLWKRDGMDFRMNIYNC
                                                                                                                                                                                                                                                                                                                                                                                                                                          SLIAKKGSKEKVKTM-LQDFLRDQRNSAVFQNIQNPLNPSFRCSGVTPDRCKVMDSKMRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKIEPRAQSEVGMMLLTRALCDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYAYPDPAVRREAIRCLH-FLKDEDLLLYLLQLVQAIKHESYLESDLVVFLLERALRNQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEQRH-VWMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLL
                                                                                                                                                                                  SWKTSLNWASH 1080
                                                                                                                                                                                                          MWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNG
                                                                                                                                                                                                                             LRKHGCLILSLFSMMISTGLPELSSEKDLDYLRETLY-LDYTEEKAREHFRAKESEALAN
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Similarity 37.0%;
                                                                                                       PRELIMINARY;
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125; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 983; DB 5; 1
Pred. No. 2.24e-163
                                 VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                PRT;
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Best Local S
Matches 20
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SUBMITTED (MAY-1996) TO EMBL/GENBAN
EMBL; US7843; G2076751; -
PROSITE; PS00915; PI3_4_KINASE_1; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PFAM; PF00454; PI3_PI4_KINASE; 1.
PFAM; PF00613; PI3K=; 1.
PFAM; PF00794; PI3K_C2; 1.
PFAM; PF00794; PI3K_C2; 1.
PFAM; PF00794; PI3K_C3; 1.
PFAM; PF00794; PI3K_C3; 1.
PFAM; PF00794; PI3K_C3; 1.
                                                                                                                                                 O70173 PRELIMINARY:
070173; PRELIMINARY:
070173; PREMBLREL 07, C
01-AUG-1998 (TREMBLREL 07, C
01-AUG-1998 (TREMBLREL 08, I
01-NOV-1998 (TREMBLEEL 08, I
01-NOV-1998 (TREMBLEEL 08, I
01-NOV-1998 (TREMBLEEL 08, I
SEQUENCE FROM N.A.
TISSUB-REGENERATING LIVER;
MEDLINE; 98184888.
ONO F., NAKAGAWA T., SAITO S., OWAD
SUZUKI M., MATSUNO S., KONDO H.;
"A novel class II phosphoinositide
                                                                                                                                                                                                                                                                                      1091
                                                                                                                                                                                                                                                                                                                  1011
                                                                                                                                                                                                                                                                                                                                                1031
                                                                                                                     RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                         SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                           F-T---L-SCAGYCVATYVLGIGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRE 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIFKNGDDLRQDMLTLQMIQLMDVLWKQEGLDLRMTPYGCLPTGDRTGLIEVVLRSDTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEQ-YLIQLVQVLKYESYLDCELTKFLLERALANRKIGHFLFWHLRSEM-HVPSVALR- 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELSCSKDIQYLKDSL-ALGKTEEEALKHFREKFNEALREGWKTKVNWLAHNV 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIF 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRQEAYLEALSHLQSPLDPSTLLAEVCVEQCTFMDSKMKPLWIMYSNEEAGSGGTV---G
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                                                                                                                                                                                                                                                                                                                                                ROPFILTEHFMTVIRSGKSVDGNSHELOKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRISTLVK-GMPKDV-A-TMKLRDE- 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.48;
Similarity 34.98;
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                                                                                                         MURIDAE;
                                                                                                          MURINAE;
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Pred. No. 2.62e-146;
135; Mismatches 199;
                                                                                                                                                                LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                               CREATED)
                                                                                                         VERTEBRATA;
E; RATTUS.
                                                                                                                                                                                                                             PRT;
                                  OWADA Y.,
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    3-kinase
                                  SAKAGAMI
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    predominantly
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                                                                                                                        EUTHERIA;
    expressed
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                                                                                                                        RODENTIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000750;
                                               BROWN R.A., HO L.K.F., WEBER-HALL S., SHIPLEY J.M., FRY M.J.;
"Identification and cDNA cloning of a novel mammalian C2
domain-containing phosphoinositide 3-kinase, HsC2-PIJK.";
BIOCHEM. BIOPHYS. RES. COMMUN. 233:537-544(1997).
-!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDXL-1D-MYO-INOSITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1113
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EMBL; AB009636; D1026564; -.

SEQUENCE 1505 AA; 170974 MW; 5ACFBC1B CRC32;
                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 97289668. BROWN R.A., HO L.K
                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
PHOSPHOINOSITIDE 3-KINASE (EC 2.7.1.137)
(1-PHOSPHATIDYLINOSITOL 3-KINASE) (PHOSPHATIDYLINOSITOL
(PI3-KINASE) (PTDINS-3-KINASE).
                                                                                                                                                                                                                                                                                        CATARRHINI;
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Local Similarity 31.6%;
Local Similarity 31.6%;
ES 181; Conservative
1-PHOSPHATIDYL-1D-MYO-
; Y11312; E311430; -.
                                                                                                                                                                                                                                                                      I3K.
SAPIENS (HUMAN).
SYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCDRHNDNIMLTKSGHMFHIDFGKFLGHAQTFGGIKRDRAPFIFTSE-MEYFITE-GGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .KWFS-Q---HNHLK----E--D-YEK-----ALRN-F-----F-YSCAGWCVVTFILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKGIDRDACSYFTSNALPLKITFINANPMGK-NI---SVIFKAGDDLRQDMLYLQIIQVM
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Pred. No. 5.04e-94;
135; Mismatches 204;
                             INOSITOL
                                                                                                                                                                                                                                                                                                                VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                          3-PHOSPHATE
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01-AUG-1998 (
01-AUG-1998 (
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PFAM; PF00787;
PFAM; PF00792;
PFAM; PF00794;
TRANSFERASE.
                                                                                                                                                                                                                                                                   01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINGSTOL 3-KINASE, C2 DOMAIN CONTAINING,
POLYPEPTIDE (PHOSPHOINOSITIDE 3-KINASE-C2GAMMA).
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PFAM;
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                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
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                                                MISAWA H.,
                                                                         MEDLINE; 98189216.
                                                                                                TISSUE-LIVER;
                                                                                                                          SEQUENCE FROM N.A.
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                              YOSHIMURA A.;
                                                                                                                                                                          SCIUROGNATHI; MURIDAE;
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'Cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWSTKTNWLFHAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYVYDALRPQ-DTEANATTYFTRLIESSL-GSVATKLNFFIHNLAQ 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -AALLCCCGKGLREEFNRQCWLVNALAKLAQQVREAAPSARQGILRTGLEEVKQFFALNG 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YE-SCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWRRYIQKQEPDLLIVLSELAFVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MAYVING-GDKPSSR-FHDFVDLCCQAYNLIRKHTHLFLNLLGLMLSCGIPELSDLEDL
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PF00454; PI3_PI4_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180;
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Similarity 30.7%;
                                                  OHTSUBO
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
  characterization
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PI3K_rbd; 1
                                                  .
                                                  COPELAND
                                                                                                                                                                          MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140;
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Pred. No. 1.13e-90;
  of.
                                                                                                                                                                                               VERTEBRATA;
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Best Local
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                                                      MEDLINE; 96278830.
MOLZ L.M., CHEN Y.W., h "Cpk is a novel class o domain.";
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061182;
01-NOV-1996
01-NOV-1996
01-NOV-1998
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BIOCHEM. BIOPHYS. RES. COMMUN. 2
EMBL; ABO08791; D1026355; -.
MGD; MGI:1203730; PIK3C2G.
SEQUENCE 1506 AA; 171579 MW;
                                                                                                                                                                                                                                                                            PIK3C2A OR CPK-M.
MUS MUSCULUS (MOUSE),
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING,
PULYPEPTIDE (PHOSPHOINOSITIDE 3-KINASE).
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 SCIUROGNATHI;
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91; U52193; ...
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  MGI:1203729; PIK3C2A
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1 Similarity 30.2%;
173; Conservative
                                                CHEM. 271:13892-13899(1996).
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                                                                                                                                                                                                                                                                 MURIDAE;
                                                                                                    of Drosophila PtdIns 3-ki
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; Pred. No. 1.
134; Mismatc
                                                                                                                                                                                                                                                                                       VERTEBRATA;
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                                                                                                       3-kinase
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Best Local
SEQUENCE FROM N.A.
MEDLINE; 94150718.
WILSON R., AINSCOUGH F
BONFIELD J., BURTON J
                                                                                                                     SWINBURNE
SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                  Q17482;
Q17482;
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01-NOV-1996 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                              EUKARYOTA; I
RHABDITINA;
                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                         AGE-1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      846 KLLDIIHR-DSSFGLSKEDKVFLWENRYYCLKH-PNCLPKILASAP-NWK-WANLAKTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-FQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPELTSIQDLKYVRDALQPQT-TDA
: :| | | | :| ::::: :||::||: ||||:: || :: :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHNDNIMLRSTGHMFHIDFGKELGHAQ-MFGSFKRDRAPFVLTSD-MAYVING-GEKPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLKEGLDLRMVIFRCLSTGRDRGMVELVPASDTLRKIQVEYG-VTGSFKD-KP--LAEWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNIKSCSFFSSNAMPLKVTMVNADPLGE-EIN--VM-FKVGEDLRQDMLALQMIKIMDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRI-SLLMEAYLRGNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSSLVRFLLSRALGNIQIAHSLYWLLK-D-A-LHDTHFGSR-YEHVLGALLSVGGKGLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLQMLVKKHESGIVLEEDEQRHVWMWRRYIQKQEPD-LLIVLSELAFVWTDRENFSELYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHSDNLMLTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMTVIRSGKSVDGNS
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PF00454;
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1 Similarity 30.1%;
172; Conserva+*...
                                                                                                                   (OCT-1995)
                                                                                                                                                                                                           METAZOA; NEMATODA; RHABDITOIDEA; RHAB
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; PI3K_rbd; 1.
58 AA; 187438
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PI3_PI4_kinase;
PI3Ka; 1.
    J.,
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  CONNELL M., COPSEY T., COOPER
                                                                                                                     EMBL/GENBANK/DDBJ
                                                                                                                                                                                                           DDA; SECERNENTEA; RHABDITIA; RHABDITIDA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 599; DB 11;
Pred. No. 2.40e-86;
137; Mismatches 210;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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    COULSON
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RESULT 10
ID 75747
AC 075747
AC 075747
DT 01-NOV-DT 01-NOV-DT 01-NOV-DT -01-NOV-DE PI3-KIN
OS HOMO SAN
OC EUKARYO
OC CATARRH
RN -[1]
RP SEQUENCI
RA ROZYCKA
SEQUENCI
DR EMBL; ASQ SEQUENCI
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Best Local S
Matches 7
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Best Local
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01-NOV-1998
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NATURE 368:32-38(1994).
NATURE 368:32-38(1994).
EMBL; Z66519; E1343409; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ROZYCKA M., BROWN R., FRY M.;
"CDNA cloning of a novel mammalian PI3-kinase.";
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ00000B; E1309758; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; ZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRAXTON M., DEAR S., DU Z., DÜRBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MIRSTEN J., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1071
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                               942
                                                                                                                                                   827
                                                                                                                                                                                                                                           637
                                                                                                                                                                                                                                                                                                      577
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                                                                                                                                                                                                                                                         ILRRWTFSQPLEALGLLTSSFPDQEIRKYAVQQLDNLLNDELLE-YLPQLYQAVKFEWNL :| :| : |: |:|:|:|:|
                                                                                                                                                                                                                                                                                                                     KHIARLSQKQ-TPLLLSEEKKRYLWFYRFYCNNENCSLPLVLGSAP-GWDER-TVSEMHT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRA
                                                                                                                                                                                                                                                                                                    KKLQMLVKKHESGIVLEEDEQRHVWWWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWSTKTNWLFHAVKHY 76
                                                                            IWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKW
                          IWLQEGLDMQMIIYRCLSTGKDQRLVQMVPDAVTLAKIHRHSGLIG-PLK--ENT-IKKW
                                                         EMIIDKAIVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDN
                                                                                                                    HIKIITRQVDMVDELT-RISTLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLG
                                                                                                                                               EFSKEQKLIKILGDIGERVKSASDHQRQEVLKKEI-GRLEEFFQDVNTCHLPLNPALCIK
                                                                                                                                                                              QSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYL-RGNEE
                                                                                                                                                                                                          ESPLVQLLLHRSLQSIQVAHRLYWLLK-N-AE-NEAYFKSW-YQKLLAALQFCAGKALND
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Similarity 100.0%;
76; Conservative
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G (TREMBLREL.
G (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                       1448 AA;
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                                                                                                                                                                                                                                                                                                                                                              Conservative
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                            Score 590; DB 4;
Pred. No. 1.40e-84;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 5.16e-83;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Matches 17
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Q61194
Q61194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
TTTTCANAMHT; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHOSPHATIDYLINOSITOL 3-KINASE, C2 DOMAIN CONTAINING,
POLYPEPTIDE (P170 PHOSPHATIDYLINOSITOL 3-KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 96278746.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. BIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRBASIUS J.V., GUILHERME A., CZECH M.P.;
Mouse p170 is a novel phosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRBASIUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 995
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                                                                                                                                                                                             637
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                                                                                                                                                                                                                                                                         699
                                                                                                                                                                                                                                                             KLLDIIHR-DSSFGLSKEDKVFLWENRYYCLKH-PNCLPKILASAP-NWK-WANLAKTYS 754
                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1203729; PIK3C2A.
WLKEGLDLRMVIFRCLSTGRDRGMVELVPASDTLRKIQVEYG-VTGSLRK--PT--SEWL
                                                                                                                                                       NSSLVRFLLSRALGNIQIAHSLYWLLK-D-A-LHDTHFGSR-YEHVLGALLSVGGKGLRE
                                                                                                                                                                                          DRHSDNIMITEDGKYVHIDFGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIIDKAIVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNI
                                                     LNIKSCSFTSSNAMPLKVTMVNADPLGE-EIN--VM-FKVGEDLRQDMLALQMIKIMDKI
                                                                                        HIKIITRQVDMVDELTRISTLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLGE
                                                                                                               ELSKOMKLVOLLGGVAEKVROASGSTROVVLOKSMERVOSFFLR-NKCRLPLKPSLVAKE
                                                                                                                                           QSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRI-SLLMEAYLRGNEE
                                                                                                                                                                                                                     LLHQWPPLCPLAALELLDAKFADQEVRSLAVSWM-EAISDDELADLLPQFVQALKYEIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARKFFAGIYEEAFNGSWSTKTNWLFHAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATSHFTKKIKESLE-CFPVKLNNLIHTLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKE 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHFQDFVELCCRAYNIIRKHSQLLLNLLEMMLYAGLPELSGIQDLKYVYNNLRPQ-DTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRHNDNIMLTKSGHMFHIDFGKFLGHAQTFGGIKRDRAPFIFTSE-MEYFITE-GGK-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRKQCGIEDEKKKSKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIK
                                                                                                                                                                                                                                                                                                                                                          PF00787; PX; 1.
PF00792; PI3K_C2; 1.
PF00794; PI3K_rbd; 1
                                                                                                                                                                                                                                                                                                                                                                                                           PF00168; C2; 1.
PF00454; PI3_PI4_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DL. CHEM. 271:13304-13307(1996).
U55772; G1305538; -.
                                                                                                                                                                                                                                                                                                                                                                                                     PF00613; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                   1509 AA;
                                                                                                                                                                                                                                                                                                6.8%;
llarity 30.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                   rbd; 1.
170777
                                                                                                                                                                                                                                                                                                Score 589; DB 11; 1
Pred. No. 2.20e-84;
136; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                   E404092B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-kinase
                                                                                                                                                                                                                                                                                                                        Length 1509
                                                                                                                                                                                                                                                                                                   Indels
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RESULT OCCURRENCE OCCU
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Matches
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SEQUENCE FROM N.A.

MEDLINE; 97479209.

DOMIN J., PAGES F., VOLINIA S., RITTENH
STEIN R.C., WATERFIELD M.D.;

"Cloning of a human phosphoinositide 3-
displays reduced sensitivity to the inh
BIOCHEM. J. 326:139-147(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1115
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EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TREMBLREL 04, 01-JAN-1998 (TREMBLREL 05, 01-NOV-1998 (TREMBLREL 08, PHOSPHOINOSITIDE 3-KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         874 KLLDILHK-DSSLGLSKEDKAFLWEKRYYCFKH-PNCLPKILASAP-NWK-WGNLAKTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EATIFFTRLIESSL-GSIATKFNFFIHNLAQ 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKE 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R-FQLFVDLCCQAYNLIRTT-NLFLNLLSLMIPSGLPELTSIQDLKYVRDALQPQT-TDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHSDNLMLTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMTVIRSGKSVDGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWI
                                                                                                                                                        ELNIKSCSFFSSNAVPLKVTMVNADPLGE-EIN--VM-FKVGEDLRQDMLALQMIKIMDK 1158
                                                                                                                                                                                                                                       EHIKIITROVDMVDELTRISTLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLG
                                                                                                                                                                                                                                                                                   ELLKQ-TKLVQLLGGVAEKVRQASGSARQVVLQRSMERVQSFFQK-NKCRLPLKPSLVAK 1102
                                                                                                                                                                                                                                                                                                                                                                                                     NSSLVQFLLSRALGNIQIAHNLYWLLK-D-A-LHDVQF-STRYEHVLGALLSVGGKRLRE 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLHQWPALYPLIALELLDSKFADQEVRSLAVTWI-EAISDDELTDLLPQFVQALKYEIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLQMLVKKHESGIVLEEDEQRHVWWWRRYIQKQEPD-LLIVLSELAFVWTDRENFSELYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00168; C2; 1.
PF00454; PI3_PI4_kinase;
PF00613; PI3Ka; 1.
PF00787; PX; 1.
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                                                                                                                                                                                                                                                                                                                                                            QSEVGMMLLTRALCDYRIGHRLFWLLRAEIARLRDCDLKSEEYRRI--SLLMEAYLRGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLEKWKPPSVAAALTLLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00792; PI3K_C2; 1.
PF00794; PI3K_rbd; 1.
NCE 1686 AA; 190736 MW;
IWKAANIDCCLNPYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKW
                                                         IWLKEGLDLRMVIFKCLSTGRDRGMVELVPASDTLRKIQVEYG-VTGSFKD-KP--LAEW 1214
                                                                                                                     EMIIDKAIVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDN
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Similarity 30.6%;
175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 590; DB 4;
Pred. No. 1.40e-84;
139; Mismatches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8BA83E82 CRC32;
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inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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934
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.2%;
Best Local Similarity 25.2%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACDOUGALL L.K., DOMIN J., WATERFIELD M.D.
"A family of phosphoinositide 3-kinases in
new mediator of signal transduction.";
CURR. BIOL. 5:1404-1415(1995).
EMBL; X92892; E211623; -.
PFAM; PF00158; C2; 1.
PFAM; PF00158; C2; 1.
PFAM; PF00613; PI3_PI4.
PFAM; PF00787; PX; 1.
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Q24453
Q24453;
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01-NOV-1998 (TREMBLREL.
PHOSPHOINOSITIDE 3-KINAS
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EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
PTERYGOTA; DIFTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00792; PI3K_C2; 1.
PFAM; PF00794; PI3K_rbd; 1.
SEQUENCE 1876 AA; 210434 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEATIFFTRLIESSL-GSIATKFNFFIHNLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRHSDNLMLTEDGKYVHIDFGHILGHGKTKLG-IQRDRQPFILTEHFMTVIRSGKSVDGN 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMNKMWLAERLDLKMVTFNC-VPTGYKSGMIELVSEAETLRK-IQVECGLTGSFK-DR--
                                                                                                                                                                                                                                                              PRYPDAKVREKAVEWIS-KMPNDQLVDFLPQLVQSLKHDTYEGSAMARFLLSKCLESPRF 1175
                                                                                                                                                                                                                                                                                                          EQRHV-WMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLG
                                                                                                                                                                                                                                                                                                                                     ERREVFWEKRLYLQSYPNALPKVLHA-AHSW-DYANLIDLHALLHSWAPLSPLQSLELLL 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEARKFFAGIYEEAFNGSWSTKTNWLFHAVKH 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHELQKFKTLCVEAYEVMWNNRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESK 1113
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 MGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSI-DPSFMNKWIRKQCGIEDEKKKSKKD
                                                            WKNKNPKSDLHLPFCAMIFKNGDDLRQDM-LVLQVLEVMDNIWK-AANIDCCLNPYAVLP
                                                                                       -PELEV-TGVSVRNCS-YF-NSNTLPLKINFVGPDAESLPAIFKCGDDLQQDQLTIQLIR 1343
                                                                                                                     TLVKGMPKDVATMKLRDELRSISHKMENMDSPLDPVYKLGEMIIDKAIVLGSAKRPLMLH
                                                                                                                                                  G-EKMLQRFMYQHRMCQKLTTIAESVKEAKESMRQKSLAAGMDEVHQDLLEQPT-CLPLG 1287
                                                                                                                                                                                GHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRIS
                                                                                                                                                                                                             GHHMYWLL-VH-S-LPD-D--PHNSIGAAMVDQEYDESQVTQVRYYRRNKMMLRALMAIC 1229
                                                                                                                                                                                                                                              KRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRI 714
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                  Score 452; DB 5;
Pred. No. 6.65e-58
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches 234;
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Best Local
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                        1230
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MEDLINE; 96362138.

MACDOUGALL L.K., DOMIN J., WATERFIELD M.

"A family of phosphoinositide 3-kinases
new mediator of signal transduction.";
CURR. BIOL. 5:1404-1415(1995).
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EUKARYOTA; METAZOA; ARTHROPODA; TRAC
PTERYGOTA; DIPTERA; BRACHYCERA; MUSC
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G-EKMLQRFMYQHRMCQKLTTIAESVKEAKESMRQKSLAAGMDEVHQDLLEQPT-CLPLG
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139; Conservative
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, LAST SEQUENCE UP
, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                       Score 446; DB 5;
Pred. No. 9.18e-57;
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MUSCOMORPHA; EPHYDROIDEA;
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Q24209;
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01-NOV-1996
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PTERYGOTA;
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                                                                                                                                                                                                                      1059 ERREVFWEKRLYLQSYPNALPKVLHA-AHSW-DYANLIDLHALLHSWAPLSPLQSLELLL 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1569
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMMBL, U52192; G1372420; --
FLYBASE; FB900015278; P13K68D.
PFAM; PF00158; C2; 1.
PFAM; PF00454; PI3_PI4_kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain.";
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; PF00792;
; PF00794;
GHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRGNEEHIKIITRQVDMVDELTRIS
                                            AHHMYWLL-VH-S-LPD-D--PHNSIGAAMVDQEYDESQVTQVRYYRRNKMMLRALMAIC 1229
                                                                                                                                           PRYPDAKVREKAVEWIS-KMPNDQLVDFLPQLVQSLKHDTYEGSAMARFLLSKCLESPRF 1175
                                                                                                                                                                                             EQRHY-WMWRRYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEKWKPPSVAAALTLLG
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                                                                                              KRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRI
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                                                                                                                                                                                                                                                                                            139;
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METAZOA; ARTHROPODA; TRACHEATA; HI
DIPTERA; BRACHYCERA; MUSCOMORPHA;
                                                                                                                                                                                                                                                                                                                                                                                           1876
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PI3K_rbd; 1.
76 AA; 210504
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25.0%;
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Pred. No. 9.18e-57;
147; Mismatches 234;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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; TRACHEATA; HEXAPODA; INSECTA;
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1131 SWSTKTNWLFHAVKH 1145
              1569 SWFTQFNFFLHNLAQ 1583
                                                1288 -PELEV-TGVSVRNCS-YF-NSNTLPLKINFVGPDAESLPAIFKCGDDLQQDQLTIQLIR 1343
                                                                                                                                                                                                                                                                                                                                   1230 G-EKMLQRFMYQHRMCQKLTTIAESVKEAKESMRQKSLAAGMDEVHQDLLEQPT-CLPLG 1287
                                                                                                                                                    1344 IMNKMWLAERLDLKMVTFNC-VPTGYKSGMIELVSEAETLRK-IQVECGLTGSFK-DR-- 1398
                                                                                                                                                                                                        893 MGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSI-DPSFMNKWIRKQCGIEDEKKKSKKD 951
                                                                                                                                                                                                                                                         835 WKNKNPKSDLHLPFCAMIFKNGDDLRQDM-LVLQVLEVMDNIWK-AANIDCCLNPYAVLP 892
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CR The sequence is that encoding the AGE-1 polypeptide. AGE-1 is capability involved in control of senescence. Reduced AGE-1 mediated signalling increases longevity complete abrogation causes developmental arrest. Agents that decrease expression or activity are used to increase longevity (delay the onset of age-related conditions) in a mammal. CR They can be used as pesticides (against insects and menatodes). CR They can be used as pesticides (against insects and menatodes). CR Since the agents target invertebrate diapause events, they are capabilities than compounds that inhibit neuro-transmission. CR Measurement of age-1 gene expression or AGE-1 protein activity can compounds that inhibit neuro-transmission. CR Le used in the determination of the longevity of an animal. CR Le used in the determination of the longevity of an animal. CR Le used in two-hybrid screens to identify proteins (potential modulators) that interact with AGE-1.

CR Sequence 3504 BP; 1069 A; 688 C; 826 G; 921 T;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 3504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGE-1 polypeptide(s) and related nucleic acid, vectors, transformed cells - and antibodies, used to determine longevity of animals and to identify modulators, potentially useful for increasing longevity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP.
MOTTIS J, Ruvkun G, Tissenbaum
WPI; 98-145603/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9805761-A1.
12-FEB-1998.
07-AUG-1997; U13914.
07-AUG-1996; US-023382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans age-1 gene.
Age-1 gene; AGE-1 polypeptide; longevity;
age-related conditions; pesticides; insect
PI3K; phosphatidylinositol-3-Kinase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V18654;
03-AUG-1998
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241 TGGTTTCTTGCAAATGTGCGAACATCGCTAGAAATCAAGCTATCAGATTTCAAACATCAA 300
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                                                                                                                                                                                                                                                                       GGTGTCGCAGATATCATCACTATGTGTCCATTCGGAGAAGTTATTAGTGTAGTATTTCCG 240
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ilarity 100.0%;
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Pred. No. 0;
0; Mismatches
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Result

Score

Query Match 100.

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Description

Caenorhabditis ele

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V18654 Q57012 Q51155

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2100 4918 110000 1612 731

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Human NPIK gene. N Human NPIK gene. N Human NPIK gene. N Human NPIK gene. N

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Sequence of the L. Continuation (15 o Aequorin gene Bios Streptococcus uber

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Bacillus thuringie Bacillus thuringie Human cystatin B g Sequence encoding Delta endotoxin g Continuation (11 o

Nematode toxin Human cystatin B Human mutant EPMI .falciparum GBP13

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cDNA encoding a hu Phosphatidyl inosi Phosphatidyl inosi Human PITR-c cDNA. Human PITR-f cDNA.

Human phosphatidyl

Porcine phosphoinc

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Human p110 cDNA. R cDNA encoding mamm

p110 cDNA. PtdIns 3-kinase Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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IDENTITY_NUC

US-08-908-453-2 3504

CGGAAGCCATGGAGCTCGAG.....ACGCAGTCAAACACTACTGA 3504

240622 seqs, 94065609 residues

Run on: OM nucleic

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen

July 16, 1999, 20:02:42 ; Search time 66.58 Seconds (without alignments) 9901.048 Million cell updates/sec

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	1140	ATTATGTGAGAGCACACGAAAACTTGCTCTAGACGTGCTCAGCGTGTCTATAGA	1081	밁
٠	1140	CATTATGTGAGAGCACACGAACGAAAACTTGCTCTAGACGTGCTCAGCGTGTCTATAGAT	1081	Qy
	1080	TCGCCGACAATCAC	1021	뭥
	1080	GCCGACAATCACTAGTCCTCAAAGACTATTGTCGCCCAAAAACCACTCTACGAACC	1021	Qy
	1020	CTTACGTCTTATGATGGTGTCCGTTCGGAACTGGAAAGCTATCGATGCCCTGGATTCGTT	961	В
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	960	GAAGGATGGTTTCTTCAATTGGCTGGACGTACCACGTTTGTTACAAATCCAGATGTCAAA	901	Б
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	780	GCCAAGCTGAGTTATCAGATGTTTTGGAGAAAACGTAAAGCGGAAATCAATGGAGTTTGC		В
	780	CCAAGCTGAGTTATCAGATGTTTTGGAGAAAACGTAAAGCGGAAATCAATGGAGTTTG	721	Qγ
	720	GAACAGTACTTGTGTTGTTGAATCGTGCCCGAAAGATTTGGAATCAAAAGTCAAAAGCCT	661	밁
	720	AACAGTACTTGTGTGTTGGTGAATCGTGCCCGAAAGATTTGGAATCAAAAGTCAAGGC	661	γQ
	660	ACGAAGAAAACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGCGTTCCCCGAA	601	Дb
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	600	AAACTGGAAGAGACCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTGGGCTCGT	541	밁
	600	TGGAAGAGAGCCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTGGGCTC	541	Qy
	540	ATAAACAGGGATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATACTCACTGGAT	481	탕
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2 23	GCCGTATCTCACTTCTGATGGAAGCTTACCTCCGTGGAAATGAAGAGCACATCAAGAT	28	? D
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22	TGGCTGCTCCGTGCAGAGATTGCTCGTTTGAGAGATTGTGATGTGAAGAGTGAAGAATAT	2221	B 5
	TIGGAATGAIGCTCTTGACTAGAGCTCTCTGCGATTATCGAATTGGACATCGACTTTT	16	, B
22	GGACATCGACTTT	2161	Qy
216	CATCTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGGAA	2101	ф
	ATCTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGG	10	Qy.
210	CGTGTGATTCGAAAGTTTGCAGTGGAGAAGTTGAAGTGAGCAGCTGAGCCCGGTCACATTC		g &
2 6	ĿĿĿŖĊŖĊijŖŎijŎijŎijŶĸŖŎijĸŎijŔĸŎijĸŖŎijĸŖŎijĸijŎŖĸŎijĸijŎŖŎijĬijĸĸŖŎijĸijĬĸijĸŖĸŖŎijĸijĸŖŖijijij ĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	2 2	O t
3 2	AAATGGAAAACGGCGGAGTGTGGCAGCCGTTGACTTTGCTTGGAAAAACGTTGCACGGAT	1981	P 04
19	GAACTCGCATTTGTGTGGAGACTGATCGTGAGAACTTTTCCGAGCTCTATGTGATGCTTGAA	1921	рь
19	AACTCGCATTTGTGTGGACTGATCGTGAGAACTTTTCCGAGCTCTATGTGATGCTTG	1921	Qy
19	GTCTGGATGTGGAGGAGATACATTCAAAAGCAGGAGCCTGATTTGCTCATTGTGCTCTCC	1861	οь
19	TCTGGATGTGGAGGAGATACATTCAAAAGCAGGAGCCTGATTTGCTCATTGTGCTCTC		Qy
18	CAGATGCTTGTCAAGAAGCATGAATCTGGAATTGTATTAGAGGAAGATGAACAACGTCAT	1801	B 4
	TGAATATTAIGGGTGATGACTATGAGTCGTGTATCAGAGATCCAGGATATAAGAAGCT	0 7) D
	TTGAATATTATGGGTGATGACTATGAGTCGTGTATCAGAGATCCAGGATATAAGAAGCTT		. Q
17	ATGCCGAGTCAAGGACAATACACATATCTCGTCAAGCACCGAAGTACTTGGACGGAAACT	1681	Db
17	TGCCGAGTCAAGGACAATACACATATCTCGTCAAGCACCGAAGTACTTGGACGGAAAC	1681	Qy
16	AGGATAGGCACCAACGCAGCGGTTACAATTGAAATCTCAAGTTATGGTGGTAGAGTTCGA	1621	Db .
16	GGATAGGCACCAACGCAGCGGTTACAATTGAAATCTCAAGTTATGGTGGTAGAGTTCG	1621	Qy
16	TTCCATCTGTGGGCTCCTGAACCGACTGCCAATCGTAGTAGGATCGGAGAAAATGGAGCA		Db
16	TCCATCTGTGGGCTCCTGAACCGACTGCCAATCGTAGTAGGATCGGAGAAAATGGAGC	1561	Qy
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⊥ 5	GTTGGGTAAATATGTCCCTAACCGATTGGAGAGATGAACTACGACAAGGACAATTTTT		Q.
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14	AAATGGAATAAGGAATGTACACTTTTGATCTATTACATGAAGGATATGCCACCATCTGCA	1381 1381	B 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT Eukaryotic cells transformed with mammalian phospholipid or protein kinase DNA - useful in assays for compounds involved in regulation and for treating cancers

PT cell growth regulation and for treating cancers

PS Disclosure; Fig 1; 71pp; English.

CC inositol (PtdIns) 3-kinase. This sequence was transformed into CC inositol (PtdIns) 3-kinase. This sequence was transformed into CC control (PtdIns) 3-kinase. This sequence was transformed into CC intheoryces pombe cells under the regulatory control of the nmt promoter in an embodiment of the invention. In the presence of thiamine the promoter is inactive and the cells carrying the PtdIns CC catalytic subunit plasmid grow as the parental strain. In the absence of thiamine the mmt promoter functions and the PtdIns 3-kinase catalytic subunit in induced. PtdIns activity is substantially CC increased under these conditions. Cellas containing constructs such as this, are useful in assays for detecting compounds involved in cell compounds for treating cancers and the formation of blood vessel
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Best Local
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Sequence
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Goode NT, Nurse PM, Parker
WPI; 94-065697/08.
P-PSDB; R46294.
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110 kD catalytic subunit; phosphatidyl inositol 3-kinase; transformation; Schizosaccharomyces pombe; nmt promoter; thiamine; PtdIns 3-kinase; assay; detection; cell growth; regulation; cancer
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                                                                    CTGCTCCGTGCAGAGATTGCTCGTTTGAGAGAGTTGTGATCTGAAAAGTGAAGAATATCGC
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  TACATTCGAAAGACCCTAGCTTTAGAT---AAAACTGAGCAAGAGGCTTTGGAGTATTTC
                                                 CATTIGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAGAAGAAGAAGCGAGAAAGTTTTTC
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                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 723;
                                                                                                                                                                                                                                                                                                                                                             Recombinant polypeptide(s) - with phosphoinositide-3 kinase activity, useful for controlling cell proliferation

Sclaim 7; Fig 9; 146pp; English.

Claim 7; Fig 9; 146pp; English.

Claim 7; Fig 9; 146pp; English.

Ca fragment of a PI3-kinase-encoding sequence and human cDNA isolated from a cDNA library constructed from mRNA isolated from the human cell line KGla. Positive clones were sequenced to give the human PI3 kinase pl10 sequence shown. This sequence has 95 percent homology with the bovine sequence. The domain encoding residues 19-100 of human pl10 is sufficient to encode the kinase which will associate with the p85 kinase subunit. The gene may be used to provide a protein with PI3 kinase activity, and is useful for screening for (ant)agonists of PI3 kinase activity which could be useful for stimulation or inhibition of cell proliferation and hence prophylaxis or therapy. Platelet or neutrophil activity or blood Sequence 3207 BP; 1028 A; 581 C; 680 G; 918 T;
                                  2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-1992; GB-008135.
(LUDW-) LUDWIG INST CANCER RES.
Dhand R, Fry MJ, Gout I, Hiles
Parkerpj, Volinia S, Waterfield
WPI: 93-351738/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist; cell proliferation; inhibition; prophylaxis; therapy; platelets; neutorphil activity; 3-phosphorylated phosphoinositides;
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Q51155;
12-APR-1994 (first ent
P110 cDNA.
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CAGTACCTAATTCAGCTAGTACAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTT
                                CTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGGAAGTT
                                                                                                   GTGATTCGAAAGTTTGCAGTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTCCAT
                                                                                                                                                                      TGGAAACCGCCGAGTGTGGCAGCCGCGTTGACTTTGCTTGGAAAACGTTGCACGGATCGT 2043
                                                                                                                                                                                                          CTGTCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGAT 1767
                                                                                                                                       TGGCCTCCAATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGATCCT
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                                                                  ATGGTTCGAGGTTTTGCTGTTCGGTGCTTAGAAAAATATTTAACAGATGACAAACTTTCT
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1. .3207
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/note= "PI3- kinase p110"
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AAAACGTTATGCGTCGAAGCCTACGAAGTAATGTGGAATAATCGAGATTTGTTCGTTTCC
                                                                                ATGACAGTGATTCGATCGGGTAAATCTGTGGATGGAAATTCGCATGAGCTACAAAAATTC
                                                                                                                                                                                  GGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCGTTTATTCTAACCGAACACTTT
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                                                                                                                                                    ATCATGGTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC
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Similarity

3.78;

Conservative

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Score 130; DB 1; Pred. No. 9.8e-29; 0; Mismatches 765;

Length 3412;

Indels

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RESULT

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Practivity, useful for controlling cell proliferation
PS Claim 7; Fig 16; 146pp; English.

CS Southern blot analysis was performed using a bovine cDNA probe contg.

CA fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC from a cDNA library constructed from mRNA isolated from the human
CC cell line KGla. Positive clones were sequenced to give the human
CC pI3 kinase pil0 sequence shown. This sequence has 95 percent
CC homology with the bovine sequence. The domain encoding residues 19-
CC 100 of human pil0 is sufficient to encode the kinase which will
CC associate with the p85 kinase subunit. The gene may be used to
CC provide a protein with PI3 kinase activity, and is useful for
CC useful for stimulation or inhibition of cell proliferation and hence
CC prophylaxis or therapy. Platelet or neutrophil activity or blood
CC glucose levels can be controlled using the kinase.
CC see also Q51155 and Q57522-3.
CC Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T;
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Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
antagonist; cell proliferation; inhibition; prophylaxis; therapy;
platelets; neutorphil activity; 3-phosphorylated phosphoinositides;
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WPI; 93-351738/44.
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PT 3-kinase-like activity, designated pilodelta - useful for controlling cell motility, particularly of metastatic cancer cells PT controlling cell motility, particularly of metastatic cancer cells PS Disclosure; Fig 9; 72pp; English.

CC The present sequence encodes a novel autophosphorylating protein controlling that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and controlling that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and controlling that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and controlling that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and controlling controlling that has PI3 (phosphatidylinositol 3-hydroxy) kinase activity, and controlling controlling metastatic cancer controlling controlling motility of cells. The protein increases motility while antisense controlling con
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(LUDW-) LUDWIG INST CANCER F
Vanhasebroeck B, Waterfield
WPI; 98-042196/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-1997;
01-JUN-1996;
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Best Local Similarity
Matches 264; Conser
New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis Claim 4; Page 27-33; 53pp; English.

This full-length composite cDNA encodes the pilo delta catalytic subunit (see W58570) of human phosphatidylinostiol 3-kinase. It was assembled from clone #249 obtained by PCR amplification (see W31341-44) of human peripheral blood mononuclear cell cDNA, clone M9528 obtained by screening a human macrophage cDNA library, and further clones obtained by RACE and PCR (see V31345-50). The following are claimed: (1) a purified and isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1998 (first entry)
Human phosphatidylinositol 3-kinase
Phosphatidylinositol 3-kinase; pl10
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                                                                                                                                                                          P-PSDB; W58570
                                                                                                                                                                                        Chantry DH, Hoekstra MF, WPI; 98-322736/28.
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25-NOV-1997; U21655.
25-NOV-1996; US-777405.
(ICOS-) ICOS CORP.
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196. .3330
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Matches 264
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Similarity 53.7%;
64; Conservative
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0; Mismatches
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ν,

Porcine phosphoinositide 30H-kinase p120 subunit cDNA.

G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
phosphoinositide 30H-kinase; p13K; signal transduction;
phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptoransgenic animal; knockout animal; inflammation; arthritis;
septic shock; adult respiratory distress syndrome; pneumonia;
asthma; allergy; reperfusion injury; atherosclerosis; cancer;
Alzhelmer's disease; cancer; antisense; ribozyme; diagnosis;

receptor;

17-AUG-1998 (first entry)

therapy;

drug screening;

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders can be identified by screening assays using a 6 protein activated PI3K, or a cultured host cell that expresses the p101 gene. Antagonists of 6 protein stimulated PI3K (acting through the p101 subunit, especially by disrupting the interaction between the p101 and p120 subunits) can be used to treat arthritis, septic shock, adult respiratory distress syndrome (ARDS), pneumonia, asthma, allergies, reperfusion injury, atherosclerosis, cancer and Alzhelmer's disease. The nucleic acids and their products can also be used for diagnosis, drug screening and clinical trial monitoring of inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pl01 and pl20 subunits - useful for diagnosis, drug screening, clinical trial monitoring and treatment of inflammatory disorders Claim 54; Fig 3A-C; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-DEC-1997.
26-JUN-1997;
27-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Braselmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
TGGAGTTGCCTGAGCTGTCGACGAAAGCCGGATTTGGATCATTTGAAGAAAACCCTCTTCT
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                                                                                                                                          ACGAAGTAATGTGGAATAATCGAGATTTGTTCGTTTCCTTGTTCACCTTGATGCTCGGAA
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nilarity 51.9%;
Conservative
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BP; 1010 A;
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Pred. No. 1.2e
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                designated PI3K-gamma and can be used as an immunogen. The enzyme, antibodies against it or nucleic acid encoding it can be used for modulating cell proliferation receptor-mediated signal transmission, histamine secretion, nerve cell differentiation, glucose transport and anti-lipolytic activity or for treating Alzheimer's disease.

N.B. Although the claimed sequences are referred to by SEQ.ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library using PCR primers corresponding to amino acid sequences KNGDDLR and HIDFG. The amplified fragment was used to probe a humar U937 cell cDNA library and several overlapping clones were isolated. The largest clone had the present sequence and coded for a protein of 1049 residues. The protein is a novel phosphatidylinositol 3-kinase (PIJSK) that differs in its regulatory mechanism from the kinase (PIJSK) that differs in the residues. The new enzyme has been known PIJK alpha and beta enzymes. The new enzyme has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page -; 10pp; German.
A 402 bp cDNA fragment was amplified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phosphatidyl:inositol 3-kinase for determn of kinase activity Claim 5; Page -; 10pp; German.
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 AGCGAGATCGTCAACCGTTTATTCTAACCGAACACTTTATGACAGTGATTCGATCGGGTA 3205
                                                   AATATGTCCACATTGATTTCGGTCACATTTTTGGGACACGGAAAGACCAAACTTGGGATCC 3145
                                                                                                                                      CGTACATAATGGGAATCAAGGATCGTCACAGTGATAATCTGATGCTCACTGAAGATGGAA 3085
                                                                                                                                                                        AAAAGTTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAA 3132
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                                   ACCTATTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTA 3252
                                                                                                      CCTTTGTTCTTGGAATAGGCGACAGACACAATGACAATATTATGATCACCGAGACAGGAA
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/product= PI3K-gamma
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Pred. No. 9.9e
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Claim 5; Page -; 10pp; German.

Claim 5; Page -; 10pp; Page -; 1
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 218; Conser
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13-OCT-1994; DE-436696.
(PLAC) MAX PLANCK GES E
Hanck T, Stoyanov B, V
WPI; 96-172545/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The enzyme, antibodies against it or nucleic acid encoding it caused for modulating cell proliferation, receptor-mediated signal transmission, histamine secretion, nerve cell differentiation, glucose transport and anti-lipolytic activity or for treating
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Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
cell proliferation; receptor-mediated signal transmission;
histamine secretion; nerve cell differentiation; glucose transport;
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                                                                                                                           3076, AAAAGTTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAA
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Sequence 4137 BP;
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Izheimer's disease.
I.B. Although the claimed sequences are referred in the claimed sequence in the control of the contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1127 A;
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                                                                                                                                                                                                                                                                   Score 86.8; DB 1;
Pred. No. 9.9e-16;
0; Mismatches 192
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AAATCCCATCGAAAAGAAGAAGATTGATAATACTCAAGCCATGAAGAAATATTTTGAAAAGTGT

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Matches

Conservative

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Indels

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Gaps

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2865

GATTCGGAAACAATGCGGAATTGAAGATGAAAAGAAGAAAAAGCAAAAAGGACTCTACGAA 2924

GCTTCCGATACCCTCAGGAAAATCCAAGTGGAATATGGTGTGACAGGATCCTTTAAAGAT 3624

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                               Query Match
Best Local
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P-PSDB; W70991.

New nucleic acid encoding phospho:inositol kinase 3-C2 alpha or its fragments - useful for, e.g. treatment of tumour cells where phenotype is associated with expression of kinase

Claim 1; Fig 1; 52pp; English.

The present sequence encodes a human class II phosphoinositide lipid The present sequence encodes a human class II phosphoinositide a class II (P13) kinase designated PIK3-C2alpha. It is characterised as a class II (P13) kinase designated PIK3-C2alpha. It is characterised murine and (P13) kinase designated PIK3-C2alpha. It is characterised as a class II (P13) kinase designated PIK3-C2alpha. It is characterised as a class II (P13) kinase designated PIK3-C2alpha. It is characterised as a class II (P13) kinase designated PIK3-C2alpha. It is characterised as a class II (P13) kinase designated PIK3-C2alpha in the conserved C2 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the conserved C3 domain found in murine and (P13) kinase designated PIK3-C2alpha in the cons
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                                                                                                                                                                                                     kinase due to the presence of a conserved C2 domain found in murine and Drosophila class II P13 kinases, its apparent lack of a p85 binding site and a substrate affinity to inositol lipids PtdIns and PtdIns(4)P. The protein has resistance to P13 kinase inhibitors Wortmannin and 1x294002. Antibodies against the protein (optionally humanised), are used to identify class II P13 kinases. Antisense sequences, antibodies or dominant negative mutants of the P13-C2alpha protein, are useful in human or veterinary medicine to block class II kinases. They can be used to treat tumour cells where the phenotype is associated with expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3256
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Domin J, Waterfield MD;
WPI; 98-427960/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a human class II P13 kinase-C2alpha.
Human; class II phosphoinositide lipid kinase; P13 kinase;
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19-OCT-1998 (first entry)
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                                                                                                                                                   P13-C2alpha
Sequence
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27-JAN-1998; G00244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIK3-C2alpha; class II; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1997; GB-001652.
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   al Similarity
179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA;
                                                                                                                                                      a protein.
5061 BP;
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                            2.0%;
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                                                                                                                                                      1634 A;
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Score 68.6; I
Pred. No. 3.2e
0; Mismatches
                                                                                                                                                      991
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                         DB 1;
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                                                        Length 5061;
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                                                                                                                                                                                                                                                                                           New isolated phospatidyl inositol-3 kinase polypeptide - used to develop products for diagnosis and therapy, particularly for proliferative disorders, e.g. inflammatory joint diseases, or cancer proliferative disorders and write (see W38756), a murine proliferative disorders and write and phosphatidyl inositol and joint phosphatidyl inositol disorders, and which are capable of phosphatidyl inositol and phosphatidyl inositol 4.5-bisphosphate, and which are involved in cell signalling cascades that control e.g. cell cycle progression and intracellular protein control e.g. cell cycle prog
                                                              Query Match
Best Local S
Matches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09731650-A1.
01-SEP-1997.
12-FEB-1997; U02193.
29-FEB-1996; US-609049.
(REGC) UNIV CALIFORNIA.
Chen Y. MOIZ L. Williams L
WFI; 97-448442/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1998 (first entry)
Phosphatidyl inositol 3-kinase cdk-m cDNA.
Phosphatidyl inositol 3-kinase; signal transduction; cell cycle; antagonist; inflammatory joint disease; cell proliferation; cance psoriasis; restenosis; atherosclerosis; therapy; diagnosis; moust
                                                                                                                                                                                          may reduce Ras activation allowing treatment of proliferative disorders such as atherosclerosis, inflammatory joint disease, psoriasis, restenosis following angioplasty, and cancer. Seguence 5285 BP; 1618 A; 1073 C; 1144 G; 1449 T
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Mus mus
2969 AATATTTTGAAAGTGTCGATCGATTCCTATACTCGTGTGTTTGGATATTCAGTTGCCACGT 3028
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                                                                                    Similarity
                                                           1.9%;
ilarity 49.5%;
Conservative
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                                                        Score 65.6; I
Pred. No. 2.6e
0; Mismatches
                                                              0
                                                           DB 1;
1.6e-09;
les 199;
                                                                                                              Length 5285;
                                                                                                                                                                                                1449 T
                                                        9;
                                                        Gaps
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This foun sequence codes for cpk (see W38757), a Drosophila CC polypeptide that belongs to a novel class of phosphatidyl inositol CC 3-kinases that contain a C2 domain, are capable of phosphotylating CC a D3 hydroxyl of an inositol ring in phosphatidyl inositol and CC phosphatidyl inositol 4-phosphate, but not in phosphatidyl inositol CC 4,5-bisphosphate, and which are involved in cell signalling cascades that control e.g. cell cycle progression and intracellular protein CC sorting. Short fragments of cpk cDNA were obtained from a Drosophila cDNA library by PCR (see T80195-96). These short CC fragments were used to screen the cDNA library to obtain larger CC fragments, and missing 5' ends were obtained by RACE. A CC recombinant host cell, transfected with a vector comprising a cpk CC nucleic acid is claimed. Novel phosphatidyl inositol 3-kinases CC can be used to screen for agonists/antagonists of activity and CC in a claimed method of treating a disorder caused by dysregulation CC of a growth factor activation signalling cascade. Antagonists of activity and classer restenosis following treatment of proliferative CC classed Ras activation allowing treatment of proliferative disorders such as atherosclerosis, inflammatory joint disease, Sequence 6831 BP; 1829 A; 1665 C; 1669 G; 1648 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1998 (first entry)
Phosphatidyl inositol 3-kinase cdk cDNA.
Phosphatidyl inositol 3-kinase; signal transduction; cell cycle; antagonist; inflammatory joint disease; cell proliferation; cance psoriasis; restenosis; atherosclerosis; therapy; diagnosis; cpk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T80200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated phospatidyl inositol-3 kinase polypeptide - used develop products for diagnosis and therapy, particularly for proliferative disorders, e.g. inflammatory joint diseases, or Example 1; Fig 9; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA. Chen Y, Molz L, Williams WPI; 97-448442/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          psoriasis; restenosis; a Drosophila melanogaster. Key Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W38757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTCCACATTGACTTTGGAAAGTTTTTGGGCCCATGCACAGATGTTTGGTAGCTTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTCCACATTGATTTCGGTCACATTTTGGGACACGGAAAGCCAAACTTGGGATCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATAATGGGAATCAAGGATCGTCACAGTGATAATCTGATGCTCACTGAAGATGGAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-609049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
148. .5778
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Length

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RESULT 14
Q57523
ID Q57523
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Best Local 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       activity, useful for controlling cell proliferation
Disclosure; Fig 20; 146pp; English.
Southern blot analysis was performed using a bovine cDNA probe contg.
a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
from a cDNA library constructed from mRNA isolated from the human
cell line KGla. Positive clones were sequenced to give the human
pris kinase pillo sequence shown. This sequence has 95 percent
homology with the bovine sequence. The domain encoding residues 19-
100 of human pillo is sufficient to encode the kinase which will
associate with the p85 kinase subunit. The gene may be used to
provide a protein with Pis kinase activity, and is useful for
screening for (ant)agonists of Pis kinase activity which could be
                                                                                                                                                                                                                                                                                                            useful for stimulation or inhibition of cell proliferation and her prophylaxis or therapy. Platelet or neutrophil activity or blood glucose levels can be controlled using the kinase. See also Q51155-6, Q59012-23 and Q57523.

Sequence 381 BP; 116 A; 78 C; 85 G; 102 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist; cell proliferation; inhibition; prophylaxis; ther platelets; neutorphil activity; 3-phosphorylated phosphoinosi
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                                                                                                                3064 CTGATGCTCACTGAAGATGGAAAATATGTCCACATTGATTTCGGTCAC
                                                                                                                                                                        3004 TGTGTTGGATATTCAGTTGCCACGTACATAATGGGAATCAAGGATCGTCACAGTGATAAT 3063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-APR-1993; G00761.
13-APR-1993; GB-008135.
13-APR-1992; GB-008135.
13-APR-1992; GB-008135.
GOUT I, HI
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Q57523 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chand R, Fry MJ, Gout Parkerpj, Volinia S, WPI; 93-351738/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PITR-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q57522 standard; cDNA; 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; R46552
                                                                                                                                                    274 TGTGCTGGATATTGCGTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATCTGATGCTCACTGAAGATGGAAAATATGTCCACATTGATTTCGGTCACATTTTGGGA 3120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGCTCAGATGTTTGGAAACTTTAAGAGAGATCGCACTCCATTTGTCCTGAC
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                                                                                   CTTTTGCTAACCAAAACAGGCAAACTCTTCCACATCGATTTCGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACATCATGTTAAAGACTTCGGGTCACTTGTTTCACATTGACTTTGGCAAGTTTCTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA.
 CDNA; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide(s) - with phosphoinositide-3 kinase
for controlling cell proliferation
                                                                                                                                                                                                                                         1.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49.8; DB 1;
Pred. No. 0.00017;
0: Mismatches 77;
                                                                                                                                                                                                                                         Score 48.8; DB 1;
Pred. No. 5.9e-05;
                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                         Length 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity, useful for controlling cell proliferation

bisclosure; Fig 21; 146pp; English.

Southern blot analysis was performed using a bovine cDNA probe contg.

a fragment of a PI3-kinase-encoding sequence and human cDNA isolated

from a cDNA library constructed from mRNA isolated from the human

cell line KGla. Positive clones were sequenced to give the human

cell line KGla. Positive clones were sequenced to give the human

riskinase pillo sequence shown. This sequence has 95 percent

chomology with the bovine sequence. The domain encoding residues 19-

100 of human pillo is sufficient to encode the kinase which will

associate with the p85 kinase subunit. The gene may be used to

provide a protein with pI3 kinase activity, and is useful for

screening for (ant)agonists of PI3 kinase activity which could be

useful for stimulation or inhibition of cell proliferation and hence

prophylaxis or therapy. Platelet or neutrophil activity or blood

glucose levels can be controlled using the kinase.

See also Q51155-6, Q59012-23 and Q57522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                J02096597-A.
09-APR-1990.
24-AUG-1984; 113000.
01-JAN-1988; JP-176125.
((CHCC) Chisso Corp.
WPI; 90-151860/20.
                                                                                                                                                                                                                                                                     Phosphoinositide kinase; PI; p85 subunit; screening; agonist; antagonist; cell proliferation; inhibition; prophylaxis; therapy; platelets; neutorphil activity; 3-phosphorylated phosphoinositides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3024 CACGTACATAATGGGAATCAAGGATCGTCACAGTGATAATCTGATGCTCACTGAAGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2964 GAAGAAATAITTTGAAAGTGTCGATCGATTCCTATACTCGTGTGTGGATAITCAGTTGC
  Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q04441 standard; DNA; 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3084 AAAATATGTCCACATTGATTTCGG
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12-APR-1994
                               P-PSDB; R04822
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Parkerpj, Volinia S,
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13-APR-1992; GB-008
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of photoprotein aequorin -
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MJ, Gout I, Hiles
Inia S, Waterfield
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Pred. No.
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2934 CGAAAAGAAGA 2944
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945 AAAAAAAAAAA 955
                                                                                                                                                                                                                          2754 TGGAATTATTGAAGTTGTGCCTAATTGTAAAACAATATTCGAGATTCAAGTTGGAACAGG 2813
                                                                                                                                                                                                                                                                                                                                                                             contg.specific DNA sequence of photoprotein aequorin Disclosure; ; Japanese. A prokaryotte host is transformed with this sequence in the prodn. of the photoprotein aequorin. The protein is useful for analysing low calcium levels.
                                                                                       2874 ACAATGCGGAATTGAAGATGAAAAGAAAAAGCAAAAAGGACTCTACGAAAAATCCCCAT 2933
                                                                                                                                                          2814 ATTCATGAATACAGCAGTTCGGAGTATTGATCCTTCGTTTATGAATAAGTGGATTCGGAA 2873
                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                     957 BP;
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Search completed: July 16, 1999, 20:56:18 Job time: 3216 sec

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1 CGGAAGCCATGGAGG
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ALIGNMENTS

œ	JOURNAL S	TITLE	AUTHORS M	REFERENCE 2	MEDLINE 9	JOURNAL N	_	TITLE A	AUTHORS M	REFERENCE 1		co.	Ħ	ORGANISM C	SOURCE C	KEYWORDS .	NID g	ACCESSION U	DEFINITION C	LOCUS	CEU56101	RESULT 1
8, Boston, MA 02114, USA	Submitted (22-APR-1996) Mol. Biol., Mass General Hospital, Wellman	Direct Submission	Morris,J.Z., Tissenbaum,H.A. and Ruvkun,G.B.	(bases 1 to 3504)	96320556	Nature 382 (6591), 536-539 (1996)	longevity and diapause in Caenorhabditis elegans	A phosphatidylinositol-3-OH kinase family member regulating	Morris, J.Z., Tissenbaum, H.A. and Ruvkun, G.	(bases 1 to 3504)	Rhabditidae; Peloderinae; Caenorhabditis.	Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;	Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;	Caenorhabditis elegans	Caenorhabditis elegans.		g1850328	U56101	Caenorhabditis elegans AGE-1 mRNA, partial cds.	CEU56101 3504 bp mRNA INV 26-FEB-1997		

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REMARK
COMMENT
FEATURES
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Matches 3504; Conserv
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                                     CTTTTCGAATTGATTGCTCCGATGAAGTGGGGAACATATTCCGTAAAGCCACAGGATTAT
                                                                                                                                                   TGGTTTCTTGCAAATGTGCGAACATCGCTAGAAATCAAGCTATCAGATTTCAAACATCAA 300
                                                                                                                                                                                                                                     GGTGTCGCAGATATCATCACTATGTGTCCATTCGGAGAAGTTATTAGTGTAGTATTTTCCG 240
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                                                                                                                            TGGTTTCTTGCAAATGTGCGAACATCGCTAGAAATCAAGCTATCAGATTTCAAACATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 3504)
Morris, J.Z., Tissenbaum, H.A. and Ruvkun, G.B.
Direct Submission
Submitted (24-FEB-1997) Mol. Biol., Mass General Hospital, Wellman
S. Boston, MA 02114, USA
Sequence and protein updated by submitter
On Feb 26, 1997 this sequence version replaced gi:1778714.
Location/Qualifiers
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WILFRAEIARLROCDLKSEEYRRISLLMEAYLRCNEEHIKIITROVDMYDELTRISTLY
KGMPKDVATMKLRDELRSISKMENMOSPLDPVYKLGEMIIDKAIVLGSAKRPLMLHW
KNKNPKSDLHLPFCAMIFKNGDDLROMLVLOYLEVMDNIWKAANIDCCLNPYAYLEM
GEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKOCGIEDEKKKSKKD
STKNPIEKKIDNTQAMKKYFESVDRFLYSCVOYSVATIMGIRKOCGIEDEKKKSKKD
VHIDFGHILGHGKTKLGIQRDROPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEA
YEVMMNRDLFYSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYE
EAFNGSWSTKTNWLEFHAVKHY"
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/translation="REMSERSDCWTRTELRRISQMHVNILHPQLQTMVEQWQMRERP
SLETENGKGSLLLENEGVADIITMCFFGEVISVVFPWFLANVRTSLEIKLSDFKHQLF
ELIAPMKWGTYSVKPQDYVFRQLNNFGELEVIFNDDQPLSKLELHGTFPMLFLYQPDG
INRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKKTCLTRGLEGTSHYAF
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DWRDELRQGQFLFHLWAPEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMPSQGQ
YTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMW
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KSLLHTFLYEMRKLDVYDTDDPADEGWFLQLAGRTTFVTNPDVKLTSYDGVRSELESY
RCPGFVVRRQSLVLKDYCRPKPLYEPHYVRAHERKLALDVLSVSIDSTPKQSKNSDMV
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/strain="N2"
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GTACTCAGCATTCGTGTTTTGTACGGAAAAGTGAAATTAAAAAGTGAAGAATTCGAAGTT 1	AAATGGAATAAGGAAATGTACACTTTTGATCTATACATGAAGGATATGCCACCATCTGCA	ATCTGC	TATGTGGGGACACTGACGCTGGCATCAAAATCTACAACAAAGTGAATGCTCAATTTGCA 1	ATTTCTGGATTCGGTTCCCGGCCGACGTGGATATGTACGTTCGAATCGAATTCAGTGTA	ACTCAAACAAGTTTCACTTTGGGACCTTGATGTGTATATTTTTTTT	AAACAAGTTTCACTTTGGGACCTTGACGCGAATCTTATGATACGGCCTGTC	AGCACACCAAAACAGAGCAAGAACAGTGACATGGTTATGACTGATTTTCGTCCGACAGCT 1	CACACCAAAACAGAGCAAGAACAGTGACATGGTTATGACTGATTTTCGTCCGACAG		attatgtgagagcacacgaacgaaacttgctctagacgtgctcagcgtgtctatagat	GTTCGCCGACAATCACTAGTCCTCAAAGACTATTGTCGCCCAAAACCACTCTACGAACCA 1	サイン にっつい きゅうけつ みつける のけつつけつ きょうきつき アボール・ボール きゅうさい ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・ファン・		tracgtetatgatggtgtccgttcggaactggaagetategatgecetggattegt	GAAGGATGGTTTCTTCAATTGGCTGGACGTACCACGTTTGTTACAAATCCCAGATGTCAAA 9	acacetttctctaceaaateceaaaatteeatetataceataceateatectecaeat	ACGTTTCTCTACGAAATGCGAAAATTGGATGTATACGATACCGATGATCCTGCAGAT	AATGAAGAATTCAAATTGAATTCAATCCGAACGAAACTCCGAAATCTCTGCT	AGAAAATGATGAAGATTCAAATTGAATTCAATCCGAAACGAAACTCCGAAATCTCTCTG	GCCAAGCTGAGTTATCAGATGTTTTGGAGAAAACGTAAAGCGGAAATCAATGGAGTTTGC 7	CCAAGCTGAGTTATCAGATGTTTTGGAGAAAACGTAAAGCGGAAATCAATGGAGTTT	GAACAGTACTTGTGTGTGGGAATCGTGCCCGAAAGATTTGGAATCAAAAGTCAAAGGCT	HACAGTACTTGTGTTGGTGAATCGTGCCCCGAAAGATTTTGGAATCAAAAGTCAAG	ACGAAGAAAACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGCGTTCCCCGAA 6	CGAAGAAAACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGCGTTCCCCC	AAACTGGAAGAGCCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTC	ACTGGAAGAGAGCCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTGGGCTC	ATAAACAGGGATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATACTCACTGGAT 5	agggataaagaattaatgagtgatataagtcattgtctaggatactcactgg	CIGICGAAATIAGAGCICCACGGCACTIICCCAATGCITTITCTCTACCAACCIGAIGGA 4	, U	
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	iii ii	GECOGIATETCACTTCTGATEGAAGCTTACCTCCGTGGAAATGAAGAGCACATCAAGA) N L	B 2
	2280 2280	1 TGGCTGCTCCGTGCAGAGATTGCTCGTTTGAGAGATTGTGATCTGAAAAGTGAAAAGT 	22	B 5
	2220 2220	1 GTTGGAATGATGCTCTTGACTAGAGCTCTCTGCGATTATCGAATTGGACATCGACTTTTC	216 216	B 8
•	2160 2160	1 CATCTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGGAA 	210 210	B 8
	2100 2100	1 CGTGTGATTCGAAAGTTTGCAGTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTC	204	g Q
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٠	1980	11 GAACTCGCATTTGTGTGGACTGATCGTGAGAACTTTTCCGAGCTCTATGTGATGCTTGAA 	192 192	ру
	1920 1920	1 GTCTGGATGTGGAGGAGATACATTCAAAAGCAGGAGCCTGATTTGCTCATTGTGCTCTCC	186 . 186	g Q
	1860 1860	1 CAGATGCTTGTCAAGAAGCATGAATCTGGAATTGTATTAGAGGAAGATGAACAACGTCAT 	180 180	P 49
	1800	1 TIGAATATIATGGGTGATGACTATGAGTCGTGTATCAGAGATCCAGGATATAAGAAGCTT 	174 174	B 8
	1740 1740	1 ATGCCGAGTCAAGGACAATACACATATCTCGTCAAGCACCGAAGTACTTGGACGGAAACT 	168 168	B 8
	1680 1680	11 AGGATAGGCACCAACGCAGCGGTTACAATTGAAATCTCAAGTTATGGTGGTAGAGTTCGA	162 162	gg vý
	1620 1620	IL TICCATCIGIGGGCICCIGAACCGACIGCCAAICGIAGIAGATGGAGCAAAAIGGAGCA	156 156	D 04
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	1500	1 GTACTCAGCATTCGTGTTTTGTACGGAAAAGTGAAATTAAAAAGTGAAGAATTCGAAGTT	144	дb

ACCESSION NID

CEY62F5 304173 bp DNA Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y62F5; HTGS phase 1.
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KEYWORDS
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                                                                            GATCITCAAGAATGGAGACGATCTTCGCCAGGACATGCTTGTTCTTCAAGTTCTCGAAGT
                                                                                                                                          AATGCTTCACTGGAAGAACAAAAATCCAAAGAGTGACCTGCACCTTCCGTTCTGTGCAAT 2615
                                                                                                                                                                                                   ACTGCGTGACGAGCTTCGATCGATTAGTCATAAAATGGAAAATATGGATTCTCCCACTGGA 2486
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                                                                                                                     AATGCATCACTGGAAGAACAAAAATCCAAAGAGTGAACTGCGCCTTCCGATCTGTGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-DEC-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 IRQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu On Dec 5, 1998 this sequence version replaced gi:3954762.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * This sequence is unfinished. When sequencing is complete, * the sequence data presented in this record will be replaced
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by a single finished sequence with the same accession
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/chromosome="II"
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Pred. No. 1.8e-134;
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A37232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 3498)
Parker, P.J., Goode, N
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SHAGLSNRLARDNELAENDKEDLAALCTRDPLSEITFDGEKDFLWSHRHYCVTI-PELLF
KLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAMELLDCNYPDPMVRGFAVRCLEKYLT
DDKLSGYLIOLVQVLKYEQYLDNLLVRFLLKKALTNORIGHFFFHLKSEMHNKTVSQ
RFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILKOEKDETOKVQMKFLVEQMR
RRDFMDALQGFLSPLNPAHQLGNLRLEECRIMSSAKRPLWLAWENDDLNSELHFQNNE
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QVIAEAIRKKTRSMLLSSEDLKLCVLEYQGKYILKVCGCDEXFLEXYPLSQYKYIRSC
IMLGRMPNLMLMAKESLYSQLPMDCFTMPSYSRISTATPYNNGETSTKSLWVINSAL
RIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLCDNVNTQRVPCSNBRWNEWINYDIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCGTTTATTCTAACCGAACACTTT
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Hiles, I.D., Otsu, M., Volinia, S., Fry, M.J., Gout, I., Dhan, R.
Panayotou, G., Ruiz-Larrea, F., Thompson, A.S., Totty, N.F.,
Hsuan, J.J., Courtneidge, S.A., Parker, P.J. and Waterfield, M.
Phosphatidylinositol 3-kinase: Structure and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M93252
g163519
phosphatidylinositol 3-kinase
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                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae;
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phophatidylinositol 3-kinase
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subunit mRNA, comp
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BASE COUNT ORIGIN Query Match Best Local Similarity Matches 723; Conserv 1888 1828 1948 2644 CAGGACATGCTTGTTCTCCAAGTTCTCGAAGTTATGGATAACATCTGGAAGGCTGCAAAC 2008 1924 CTCGCATTTGTGTGGACTGATCGTGAGAACTTTTCCGAGCTCTATGTGATGCTTGAAAAA 1983 TGGAAACCGCCGAGTGTGGCAGGCCGCGTTGACTTTGCTTGGAAAACGTTGCACGGATCGT ACCCGACAAGTTGACATGATGATGAGCTCACACGAATCAGCACTCTTGTCAAAGGAATG GGAATGATGCTCTTGACTAGAGCTCTCTGCGATTATCGAATTGGACATCGACTTTTCTGG CAGTACCTAATTCAGCTAGTACAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTT CAAGATATGCTAACCCTTCAGATTATTCGCATTATGGAAAATATCTGGCAAAATCAAGGT AAGAGTGACCTGCACCTTCCGTTCTGTGCAATGATCTTCAAGAATGGAGACGATCTTCGC GCCATCGTCCTAGGAAGTGCAAAACGTCCGTTAATGCTTCACTGGAAGAACAAAAATCCA CGTATCTCACTTCTGATGGAAGCTTACCTCCGTGGAAATGAAGAGCACATCAAGATCATC CTGCTCCGTGCAGAGATTGCTCGTTTGAGAGATTGTGATCTGAAAAGTGAAGAATATCGC CTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGGAAGTT GTGATTCGAAAGTTTGCAGTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTCCAT TGGCCTCCAATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGATCCT CTGTCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGAT 1767 ATGTCAGAATTACTCTTTCAGAACAATGAGATCATCTTTAAAAATGGGGATGATTTACGG TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAGAACCCAGACATC CAGGGCTTTCTGTCTCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAG GAAAATATGGATTCTCCACTGGATCCTGTGTACAAACTGGGTGAAATGATAATCGACAAA GAAAAGCTCATTAACTTGACTGACATTCTCAAACAAGAGAAGAAGGATGAAAACACAAAAG CATTTAAAATCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTTGGAG **GTGAGATTTTTACTCAAAAAAGCGTTAACTAATCAAAGGATCGGTCACTTTTTCTTTTGG** ATGGTTCGAGGTTTTGCTGTTCGGTGCTTAGAAAATATTTAACAGATGACAAACTTTCT TCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGGCAAGTTGAGGCTATG 1028 Conservative RIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLCDNVNTQRVPCSNPRWNEWLNYDIY
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RESULT 5 CEB0334/c REFERENCE AUTHORS 밁 δõ 밁 Š 밁 Š 밁 Š 밁 δÃ 용 Š 밁 Š 밁 Š 밁 δÃ 밁 Š 밁 Š 밁 Ş δÃ SOURCE NID DEFINITION 밁 В KEYWORDS ACCESSION LOCUS 3364 3304 2941 3244 3184 2821 3124 2761 3064 2701 3004 2641 2944 2598 2704 3178 CACACAATTAAGCA 3484 CACGCAGTCAAACA 3497 ATGACAGTGATTCGATCGGGTAAATCTGTGGATGGAAATTCGCATGAGCTACAAAAATTC GAAGTTGTGCCTAATTGTAAAACAATATTCGAGATTCAAGTTGGAACAGGATTCATGAAT ATTGATTGCTGTTTGAACCCGTACGCAGTTCTTCCAATGGGAGAAATGATTGGAATTATT AAAACGTTATGCGTCGAAGCCTACGAAGTAATGTGGGAATAATCGAGATTTGTTTCGTTTCC GCTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCTACCAAAACGAATTGGCTCTTC CATTTGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAGAAGAAGCGAGAAAGTTTTTC CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGATGATATTGCA TTGTTCACCTTGATGCTCGGAATGGAGTTGCCTGAGCTGTCGACGAAAGCGGATTTGGAT CAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGGCAGCATGCCAATCTCTTCATAAAT GGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCGTTTATTCTAACCGAACACTTT ATCATGGTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCAC CTGATGCTCACTGAAGATGGAAAAATATGTCCACATTTGATTTCGGTCACATTTTTGGGACAC CTCAAAGACAAGAACAAGGGGGAAATATATGATGCGGCCATCGATTTGTTTACACGATCA CTTGATCTTCGAATGTTACCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC ATGAAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAAATGGATTGGATCTTC TACATTCGAAAGACCCTAGCTTTAGAT---AAAACTGAGCAAGAGGCTTTGGAGTATTTC TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAAGACAAGAATTTGAGAGGTTT ATTGAAGATGAAAAGAAGAAAAGCAAAAAGGACTCTACGAAAAATCCCCATCGAAAAGAAG ACAGCAGTTCGGAGTATTGATCCTTCGTTTATGAATAAGTGGATTCGGAAACAATGCGGA GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCAGTGTAAAGGAGGCCT------Caenorhabditis elegans Z66519 HTG; Gonadotrophin-releasing hormone receptor like protein; oxalyl-CoA decarboxylase; Phytoene synthase precursor; Potassium channel protein; Yeast hypothetical protein L8167.12 11ke protein caenorhabditis elegans. Wilson, R., Ainscough, R., Anderson, K., Baynes, C Bonfield, J., Burton, J., Connell, M., Copsey, T., Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; 1 (bases 1 to 41812) g1044812 ----GAAAGGTGCACTGCAGTTTAACAGCCACACACTCCATCAGTGG 3191 DNA cosmid в0334, complete Baynes, C., ANI Rhabditia; sequence Berks, M., Caenorhabditis Rhabditida; protein. 3483 3117 3423 3303 3243 3060 3363 2760 3063 2640 2883 2823 3177 2940 3183 2820 3123 2700 3003 2943 2598

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MEDLINE
REFERENCE
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Submitted (27-0CT-1995) Louis, MO 63110, USA. E-mail:
Jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone B0334. The true right end of clone W02B12 is at 4181 in this sequence. The start of this sequence (1. 104) overlaps with the end of sequence Z66521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note IMPORPANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://webace.sanger.ac.uk/cgi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /display?db=wormace&class=Sequence &object=B0334
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YSIDDCYFSFISFATVGFGDKVPQIDTFEKFCKVITYLVWGTILNIMLISYVTNWFTQ
                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(4176. .4394,4819. .4966,5021. .5529,5685. .5735))
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for a small
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EMBL:D71591 comes from this gene; cDNA EST EMBL:D66565 comes from this gene; cDNA EST EMBL:D73312 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST EMBL:D68660 comes from this gene; cDNA EST EMBL:D68660 comes from this gene; cDNA EST EMBL:D35993 comes from this gene; cDNA EST EMBL:C11330 comes from this gene; cDNA EST EMBL:C113447 comes from this gene; cDNA EST EMBL:C11140 comes from this gene; cDNA EST EMBL:C1140 comes from this gene; cDNA EST EMBL:CNA EXT EMBL:CNA EXT EMBL:CNA EXT EMBL:CNA EXT EMBL:CNA EXT EMB
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GRPGAVYVDLPGNLVLTSTEEEISFPPOVPLFAPVSIPPIAEIEKAIDTLKSAKKPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(10596. .13851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10596. .13193)
/gene="B0334.3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Transthyretin-like family; cDNA EST EMBL:D66717 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(6522. .6659,7308. .7435,7482. .7635))
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                                                                                                                                                              complement(14352. .16202)
/gene="80334.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(10596. .11180,11230. 12857. .13062,13145. .13193))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPGAVYVDLPGNLVLTSTEEELSFPPQVPLPAPVSIPPIAEIEKAIDTLKSAKKPLV
IVGKGAAWSERGATQVQQFLTKSKLPWLATPGGKGVASDLHPRFIGQARSLALREADT
VFLIGARFNWILHFGLPPRFQKDVKVVQIDICPEEFHQNVKTEVPLLGDIGETLAELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSSTRFIASSLANVTSRRSVSLLVRRSQFSFAPQRGLISVIDKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MRQLLLLALFVSAASAFPFIGSVQAVRVTGKVTCNGQPAENIKV
KLYEKEIVLDKLLDEKSTDGRGSFTLAGNKKELTAIDPHVNIYHKCNYNGVCYKKLKI
                                                                                                                                                                                                                                                                                        ADHWLTRSKM'
                                                                                                                                                                                                                                                                                                                                               VVQGDSAFGFSAMELETIARYNLPVVTVIINNSGIYRGLLPEDDKAIEGDRTLALPVL
SLTAECRYEEMCKAFGGAGTVVRTVPEIKAALEKAFQKTDGPTVINALISTDSERKPÇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVINEGANIMDIGRIMMPSRLPKRRLDAGTFGIMGVGHGFSLAAALWARDHSPKTKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRLGDWTYDESTEWFKKLRENAEKNRAAVEKFVDDHSTPLNYYAAYQPIREFLANNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFLIGARFNWILHFGLPPRFQKDVKVVQIDICPEEFHQNVKTEVPLLGDIGETLAELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVGKGAAWSERGATQVQQFLTKSKLPWLATPGGKGVASDLHPRFIGQARSLALREADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: D36315 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADHWLTRSKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTAECRYEEMCKAFGGAGTVVRTVPEIKAALEKAFQKTDGPTVINALISTDSERKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVINEGANTMDIGRTMMPSRLPKRRLDAGTFGTMGVGHGFSLAAALWARDHSPKTKVL
VVQGDSAFGFSAMELETIARYNLPVVTVIINNSGIYRGLLPEDDKAIEGDRTLALPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRLGDWTYDESTEWFKKLRENAEKNRAAVEKFVDDHSTPLNYYAAYQPIREFLANNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:C12333 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12857. .13062,13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(10596. .11180,11230. .12189,12420. .12524,
12857. .13062,13803. .13851))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIPKSFISEGETADRTFDIGELNLAGSFSGESTDCLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="B0334.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Thiamine pyrophosphate enzymes; cDNA
EMBL:D36315 comes from this gene; cDNA EST EMBL:D33464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="B0334.3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to oxalyl-CoA decarboxylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:g3873742"
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.16202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .12189,12420. .12524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
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note="cDNA EST yk524g6.5 comes from this gene; cDNA EST

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SLNFCLYCVVSKRYRTLMKQTLKKFLHKLEGVDHPFQINLKQTKSSSAHVTSLEDHHA
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join(35963 .36144,36794..36939,37888.
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VRPALAATGATTDYIIKTIEKNNYDIYSPHLQRRNPLLLWSLLVRKLCSKY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to phytoene synthase precursor; cDNA EST
yk340f7.3 comes from this gene; cDNA EST yk340f7.5 come.
from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Yeast hypothetical protein L8167.12 like; cDNA EST CEMSG11F comes from this gene; cDNA EST EMBL:T00738 comes from this gene; cDNA EST EMBL:T00739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Translation="MKIIWVTLLLLVPQLFATQDIDEEFTHENVWKDPNDPTSGESPPASKRLLSVRNQVQKFQPDQSLRLITLRQLHEFKLDYHLEGSIKKOVQIKISRHSMSVLSKYLKNDEADLAEEREAVRSALSNIESVKPAPADRTWQDFTFVTLQPFIFTLNIFILPAAAAFVVLRSIVRPRNFWILVLSTALLVSMYSGYSKKYQEAESRRFAQFQEHAHDSCATE
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WKDAISSIYGISPLPVPRQPVAIALCSFAAGANSDMLLKLVETRQSTIGDRQFSDINA
LCEYGKSTIGSLLCLQIDALARNSPETKVLPMAYDVAKDLGAAYAIANMIRATHPLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(16591. .16664,16715. .16815,16867. .17048,17094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLDGEPPQQPAPQLLITAKEMKRLEQARNKKPEMISYPTSEREDVVSGSENGNEKKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLSRMVEILASPFQYRQKSKCLKYIESQTISIFHEISIIEVFSETISGGFFAFFSGS
AKHFNLFFRNLYDGAPLIAQIVMTIFLVLMLGAIRTPFFSYEPIWLNFCSSSIGKIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="B0334.6"
/note="e:---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17730
                                                                                                                                                                    /gene="B0334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene-"B0334.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yk383h4.3 comes
                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="similar to Gonadotropin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="B0334.6"
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/translation="mwnnrdlfyslfTlmlgmelpelsTkadldHlkKTlfCngeske
EARKFFAGIYEEAFNGSWSTKTNWLFHAVKHY"
1 7729 c 7485 g 13540 t
                                                                                                                                                                                                                       /note-"cDNA EST CEMSC28F comes from this gene; cDNA EST comes from this gene; cDNA EST yk360d11.3 comes from this gene; cDNA EST yk360d11.5 comes from this gene; cDNA EST yk355b7.3 comes from this gene; cDNA EST yk355b7.5 comes from this gene; cDNA EST yk302a12.3 comes from this gene; cDNA EST yk302a12.3 comes from this gene; cDNA EST yk302a12.5 comes from this gene; cDNA EST yk300g10.3 comes from this gene; cDNA EST yk3040.3 comes from this gene; cDNA EST yk102d4.3 comes from this gene; cDNA EST yk192d4.5 comes from this gene; cDNA EST yk192d4.5 comes from this gene; cDNA EST yk192d4.5 comes from this gene;
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/gene="age-1"
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TYVSNKNVSEFTYINEITTMIF"
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SSYFLMSLKTHMSPTTRKLQQKFFIDMIFQVSMPVVVIVLPMIYCFYSIVWQQYNQMF
NNIAIMCISLHGMCSTITMICLNPTYRHFTLSVLTCFYYDPTLRRSSVMTVSPATVTQ
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CLVLSNKYTEVAILETPSKAALLRNKPVEIYARAIYPYNRKNIRHWIEGHVSDKPHHL
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/gene="B0334.10"
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/db_xref="PID:e1343409"
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40744 ATTTGTTTTTTTTCAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAGAAGAAGAAGCGAGAA 40685 3416 AGTTTTTCGCTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCTACCAAAACGAATT 3475 3356 ATTTGGATCATTTGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAGAAGAAGAAGCGAGAA 3415 AGTTTTTCGCTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCTACCAAAACGAATT Conservative 4.0%; 96.0%; 0; Score 139.4; DB 3; Pred. No. 2.4e-25; Mismatches 6 Length 41812; Indels 0; Gaps 40625

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 3452)
Chang, H. W., Aoki, M., Fruman, D., Auger, K.R., Bellacosa, A., Tsichlis, P.N., Cantley, L.C., Roberts, T.M. and Vogt, P.K.
Transformation of chicken cells by the gene encoding the AF001076 3452 bp mRNA VRT 08-JUL-1997 Gallus gallus phosphoinositide 3-kinase catalytic subunit mRNA, complete cds.
AF001076 Tsichlis, P.N., Cantley, L.C., Roberts, T.M. au Transformation of chicken cells by the gene subunit of PI 3-kinase

catalytic

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                                                          AATTGTAAAACAATATTCGAGATTCAAGTTGGAACAGGATTCATGAATACAGCAGTTCGG
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Chang, H.W., Aoki, M. and Vogt, P.K.
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RIRILGATYNNVNIRDLDKIYVETGIYIGGEPLCDNVNTQRVPCSNPRNNEWLSYDMY
IPDLPRAARCLSICSYKGRKGAKEBEHOPLARGNINNFDYTDTLVSGKRALNLWAVPH
GLEDLLNPIGVTGSNPNKETPCLELEFDWFSNPVKFPDMTVIEEHANWTISRELGFNY
SYAGLSNRIARDNELRESDKEQLRAICTRDPLSSITEGEKDFLWSHRHYCVNTPEILF
KLLLSYKWNSRDEVAGWYCLVKUMPPDFIXFEGAMELLDCNYPDPWYRAFRYNCLEKYLF
DKLLSYKWNSRDEVAGWYCLVKUMPPIXFEGAMELLDCNYPDPWYRAFRYNFCLEKYLF
DRKLSOYLIQLVQVLKYEQYLDNQLVRFLLKKALTNQRIGHFFFWHLKSEMHNKTVSQ
RFGLLLESYCRAGMYLKHLSROYEAMEKLINLTDLKGKNEDTGKVQMKFLVEQMR
RPDFMDALQGFISPLNPAHQLGNIRLEECRINSAKRPLMUNENDDLMSELLFQNNE
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DRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDFLIVISKGAQECT
KTREFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIAYIRKTLALDK
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SRALYVCPPNVESSPELPKHIINKLDKGQIIVVIMVIVSPNNDKQKYTLKINHDCVPE
QVIABAIRKKTRSMLLSSEQLKLCVLBYQGKYILKVCGCDEYLLEKYPLSQYKYIRSC
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/db_xref-"PID:92245506
/translation-"wepresserWGIHLMPPRILVECLLPNGMIVTLECLREATLLT
/translation-"wepresserWGIHLMPPRILVECLLPNGMIVTLECLREATLLT
IKHELFKEARKYPLYQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLKVI
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/gene="c-p3k"
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/db_xref="taxon:9031"
/tissue_type="brain"
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                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1068)
Volinia,S., Hiles,I., Ormondroyd,E., Nizetic,D., Antonacci,R., Rocchi,M. and Waterfield,M.D.
Molecular cloning, cDNA sequence, and chromosomal localization the human phosphatidylinositol 3-kinase pl10 alpha (PIK3CA) gen Genomics 24 (3), 472-477 (1994)
Direct Submission
Submitted (16-DEC-1993) Stefano Volinia, Receptor Studies, Ludwig
Institute for Cancer, Research, 91 Riding House Street, London, WIP
                                                      2 (bases 1 to 3424) Volinia, S.
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RPDFMDALQGLLSPLNPAHQLGNLRLKECRIMSSAKRPLMLNWENPDIMSELLFQNNE
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KLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAMELLDCNYPDPMVRGFAVRCLEKYLT
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SRAMYYYPPHYESSPELPKHIYNKLDRGQIIYVIWYIYSPNNDKQKYTLKINHDCYPE
QVIAEAIRKKTRSMLLSSEQLKLCYLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSC
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/db_xref-"SWISS-PROT:942336"
/translation-"MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVT
/TRANSLATION-"MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVT
/TRHELFKEARKYPLHQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLKVI
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                                                                                                                                                 1720 CTGTCTGTTAAATGGAATTCTAGAGATGAAGTAGCCCAGATGTATTGCTTGGTAAAAGAT 1779
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2044 GTGATTCGAAAGTTTGCAGTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTCCAT 2103
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Molecular cloning, cDNA sequence, and chromosomal localization of the human phosphatidylinositol 3-kinase pll0 alpha (PIK3CA) gene Genomics 24 (3), 472-477 (1994)
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Submitted (16-DEC-1993) Stefano Volinia, Receptor Studies, Ludwig
Institute for Cancer, Research, 91 Riding House Street, London, W1P
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Vertebrata;
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rtebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1068)
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DRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDFLIVISKGAQECT
KTREFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIAYIRKTLALDK
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RPDFMDALQGLLSPLNPAHQLGNLRLKECRIMSSAKRPLMLNMENPDIMSELLFQNNE
LIFKNGDDLRQDMLTLQIIRIMENIMQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLEDLLNPIGVTGSNPNKETPCLELEFDWFSSVVKFPDMSVIEEHANWSVSREAGFSY
SHAGLSNRLARDNELRENDKEQLKAISTRDPLSEITEQEKDFLWSHRHYCVTIPEILP
KLLLSVKWNSRDEVAQMYCLVKDWPPIKPEQAMELLDCNYPDPMVRGFAVRCLEKYLT
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IMLGRMPNLKMMAKESLYSQLPMDCFTMPSYSRRISTATPYMNGETSTKSLMVINRAL
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EPVGNREEKILNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPH
SRAMYVYPPHVESSPELPKHIYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE
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/db_xref="SWISS-PROT:P42336"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                  3.7%; Score 130; DB 41;
45.7%; Pred. No. 5.3e-23;
vative 0; Mismatches 765;
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2824 ACAGCAGTTCGGAGTATTGATCCTTCGTTTATGAATAAGTGGATTCGGAAACAATGC	Qy
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2437 CAAGATATGCTAACACTTCAAATTATTCGTATTATGGAAAATATCTGGCAAAATCAAGG	Db
AGGACATGCTTGTTCTAAGTTCTCGAAGTTATGGATAAC	Qy
2584 AAGAGTGACCTGCACCTTCCGTTCTGTGCAATGATCTTCAAGAATGGAGACGATCTTCG	do Vo
2317 TGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAGAACCCAGACATC	Db
2524 GCCATCGTCCTAGGAAGTGCAAAACGTCCGTTAATGCTTCACTGGAAGAACAAAAATCC	Qy
2464 GAAAAHTIGGATICUTCCACTIGGATICUTGTACAACTIGGTIGAAATGATTGATCAACAAATGATTGATCAACAACTAGGTIGAAATGATAAATGATAAAGAGAG 1 1 1 1 1 1 1 1 1	B 2
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2404 CCAAAAGATGTTGCTACGATGAAACTGCGTGACGAGCTTCGATCGA	Qy
2140 GAAAAGCTCATTAACTTAACTGACATTCTCAAACAGGAGGAAGGA	Db
2344 ACCCGACAAGTTGACATGGTTGATGAGCTCACACGAATCAGCACTCTTGTCAAAGGAATG	Qy
2080 TCCTATTGTCGTGCATGTGGGATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGCAATG	В
2284 CGTATCTCACTTCTGATGGAAGCTTACCTCCGTGGAAATGAAGAGCACATCAAGATCAT	Qy
020	D D
2224 CTGCTCCGTGCAGAGATTGCTCGTTTGAGAGATTGTGATCTGAAAAGTGAAGAATATCG	Qy
1960 GTGAGATTTTTACTGAAAGAAAGCATTGACTAATCAAAGGATTGGGCACTTTTTCTTTTG	D D
2164 GGAATGATGCTCTTGACTAGAGCTCTCTGCGATTATCGAATTGGACATCGACTTTTCTG	VΩ
1900 CAGTATTTAATTCAGCTAGTACAGGTCCTAAAAATATGAACAATATTTGGATAACTTGCTT	B &
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AF001075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3389)
Chang, H.W., Aokil, M. and Vogt, P.K.
Direct Submission
Submitted (23-APR-1997) Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang, H.W., Aoki, M., Fruman, D., Auger, K.R., Bellacosa, A., Tsichlis, P.N., Cantley, L.C., Roberts, T.M. and Vogt, P.K. Transformation of chicken cells by the gene encoding the catalytic subunit of PI 3-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avian sarcoma virus 16.
Avian sarcoma virus 16
Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses
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BCC-239, La Jolla, CA 92037, USA
Location/Qualifiers
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                                        /product="gag-v-phosphoinositide 3-kinase catalytic subunit fusion protein" subunit fusion protein" /db_xref="pID:g245503" /translation="QQLIRTAPSTLTTPGEIIKYVLDRQKASHLMPPRILVECLLPNG MIVTLECLREATLLTIKHELFKKARKYPLYQLLQDESSYIFVSVTQEAEREEFFDETR
RLCDLRLFQPFLKVIEPVGNREEKILNRKIGFAIGMPICEFDMVKDPEVQDFRRNILN
VCKEAVDLRDANAPHSRALYVCPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNND
                                                                                                                                                                                                                                                                              /note="fusion gene
/gene="gag-v-p3k"
                                                                                                                                                                                                                                                                                                                                                  /organism="Avian sarcoma
/db_xref="taxon:60629"
                                                                                                                                                                            /gene="gag-v-p3k"
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                                                                                                                                        CAAGCCATGAAGAATATTTTGAAAGTGTCGATCGATTCCTATACTCGTGTGTTGGATAT
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TGTGTCGCTACCTTTATACTGGGCATTGGTGATCGCCACAACAGTAACATCATGGTGAAA
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                                            TCAGTTGCCACGTACATAATGGGAATCAAGGATCGTCACAGTGATAATCTGATGCTCACT
                                                                                           AACAAAGGAGAAATGTATGATGCAGCTATTGACTTGTTTACACGTTCTTGTGCTGGCTAC
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                                                                                                                                                                                          -AAAGGGAGCATTGCAGTTCAACAGCCATACATTGCATCAGTGGCTCAAGGACAAG
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WVAAFAVRCLEKYLTDKLSQYLIQLVQVLKYEQYLDKQLVFELKKALTNQRIGHFF
FWHLKSEMHNKTVSQRELLLESYCFACGMYLKHLSRQVEAMEKLINLTDLIKQEKKD
ETQKVQMKFLVEQMRRDPMDALQGFISPLNPAHQLGNURLEECRIMSSAKRPLWLNW
ENDDINSELLFQNNEIIFKNGDDLRQDMTLQIIRMENIWOGLDLRMLPYGCLSI
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GEATAKSLWTINSALRIRILCATYVNVNIRDIDKIYVRTGIYHGGEPLCDNVNTQRVP
CSNPRWNEWLSYDMYIPDLPRAARLCLSICSVKGRKGAKEEHCPLAWGNINMFDYTDT
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SCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLT
QDLLIVISKGAQECTKTREFERFQEMCHKAYLAIRQHANLFINLFSMMLGSGMPELQS
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/db_xref="PID:g2245504"
/translation="MARNSS"
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EHANWTISRELGFNYSYAGLSNRIARDNELRESDKEQLRAICTRDPLSEITEQEKDFL
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/note="sequence
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Catalytic Activity of the pl10-alpha Subunit of Human
Phosphoinositide 3'-Hydroxykinase is Required for Signal
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Human phosphoinositide 3'-hydroxykinase
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/translation-"MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLIT IRHELFREARKYPLHQLLQDESSYIFVSVTQEAEREEFFDETRELCDLEALGPFLKVH EPVGNREEKILLNREIGFALGMPVCEFDMYKDFBVPVDFFRHLLANCKEAVDLRDLKSPH SRAMYVYPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE
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subunit"
                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                            /codon_start=:
                                                                                                                                                            'function="phospholipid kinase"
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2284 CGTATCTCACTTCTGATGGAAGCTTACCTCCGTGGAAATGAAGAGCACATCAAGATCATC 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1984 TGGAAACCGCCGAGTGTGGCAGCCCCGTTGACTTTGCTTGGAAAACGTTGCACGGATCGT 2043
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                                                    CATTTAAAATCTGAGATGCACAATAAAACAGTTAGCCAGAGGTTTGGCCTTGTTGGAG
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                                                                                                       CTGCTCCGTGCAGAGATTGCTCGTTTGAGAGATTGTGATCTGAAAAGTGAAGAATATCGC
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                                                                                                                                                                                                                                                                                                                     CTTTTCATATTGCCTCTCATACAGGCGTTGAAGTACGAACCGCGTGCTCAATCGGAAGTT 2163
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Catalytic Activity of the pl10-alpha Subunit of Human
Phosphoinositide 3'-Hydroxykinase is Required for Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioorg. Med. Chem. (1996) In 2 (bases I to 3207) Stirdivant, S.M., Ahern, J., Cc Oliff, A. and Heimbrook, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-NOV-1996) Cancer Research, M Sumneytown Pike, West Point, PA 19486, USA
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KILLSVKWNSRDEVAQNYCLVKDWPPIKPEQAWELLDCNYDDFWVRGFAVRCLEKYLT
DDKLSOYLIOLVQVLKYEQYLDNLVARFLIKKALTNQRIGHFFFWHLKSEMHNKTVSQ
RFGLLLESYCRAGMYLKHLNRQVEAMEKLINLTDILKGEKKDETQKVQMKFLVEQMR
RDFMDALQGFLSFLNPAHQLGNLRLEECRINSAKRPLMLNWEPDIMSELLFQNNE
RDFMDALQGFLSFLNPAHQLGNLRLEECRINSAKRPLMLNWEPDIMSELLFQNNE
IIFKNGDDLRQDMLTLQIIRIMENIWQNGGLDLRMLFYGCLSIGDCVGLIEVVRNSHT
IMQIQCKGGLKGALQFNSHTLHQWLKDNNKGEIYDAAIDLFTRSCAGYCVAFFILGIG
DRHNSSIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTODFILVISKGAQGECT
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QVIABAIRKKTRSMLLSSEQLKLCVLEYQGKYILKVOGCDEYELEKYPLSQYKYIRSC
IMLGRMPNLMLMAKESLYSQLPMDCFTMPSYSRKISTATPYMNGETSTKSLWYINSI
RIKILCATYVBVNIRDIKIYVRTGIYHGGEPLCDNVNTQRVPCSNPRWNEWLNYDIY
IPDLPRAARLCLSICSVKGRKGAKEEHCPLAMGNINLFDYTDTLVSGKMALNLMPVPH
GLEDLLNPIGYTGSNPNKETPCLELEEDWFSSVVKFPDMSVIBEHANNSVSREAGFSY
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/db_xref="taxon:9606"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha;
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KIippel,A., Escobedo,J.A., Hirano,M. and
The interaction of small domains between
phosphatidylinositol 3-kinase determines
Mol. Cell. Biol 14, 2675-2685 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-NOV-1993) Anke Klippel-Giese, CVRI and Dailchi
Research Center, University of California San Francisco, 505
Parnassus Ave, Long Hospital, San Francisco, CA 94143, USA
Location/Qualifiers
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Mus musculus Balb/c
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                                                                                                                                                                       SHTGLSNRLARDNELRENDKEQLRALCTRDPLSEITEQEKDFLWSHRHYCVTIPEILP
KLLLSYKWNSRDEVAQWYCLVKDWPPIKPEQAWELLDCNYDDPWYRSFAYRCLEKYLT
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RFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILKOEKKDETQKVQWKFLVEQMR
QPDFMDALQGFLSPLNPAHQLGNLRLEECRIMSSAKRPLWLNWENPDIMSELLFQNNE
                                                                                                                                                                                                                                                                                                                                                         QVIAEAIRKKTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSC
IMLGRMPNLMLMAKESLYSQLPIDSFTMPSYSRRISTATPYMNGETSTKSLWVINSAL
RIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLCDNVNTQRVPCSNPRWNEWLNYDIY
                                                                                                  DRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPFVLTQDFLIVISKGAQEYT
                                                                                                                                                                                                                                                                                                       IPDLFRLARLCLSICSVKGRKGAKEEHCPLAWGNINLFDYTDTLVSGKWALNLWPVPH
GLEDLLNPIGVTGSNPNKETPCLELEFDWFSSVVKFPDMSVIEEHANWSVSREAGFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKHELFREARKYPLHQLLQDETSYIFVSVTQEAEREEFFDETRRLCDLRLFQPFLKVI
EPVGNREEKILNREIGFVIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPH
                                                                       KTREFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIAYIRKTLALD!
                                                                                                                          IIFKNGDDLRQDMLTLQIIRIMENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHT
IMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRSCAGYCVATFILGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                         SRAMYVYPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="phosphatidylinositol 3-kinase 110 kDa subunit"
/db_xref="PID:g414995"
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/strain="Balb/c"
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enzyme activity
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3-kinase 110 kDa subunit
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RESULT 1
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                                                                         CDS
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                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus j
delta mRNA, co
U86587
                                                                                                                                                                                  Submitted (22-JAN-1997) Biological Michigan, 3323 MSRB III, Box 0636,
                                                                                                                                                                                                                      2 (bases 1 to 3132)
Vojtek, A.B. and Cooper, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                              Chantry,D., Vojtek,A., Kashishian,A., Holtzman,D.A., Wood,C., Gray,P.W., Cooper,J.A. and Hoekstra,W.F. pllddelta. a novel phosphatidylinositol 3-kinase catalytic subunit that associates with p85 and is expressed predominantly in
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse
                                                                                                                                                                                                                                                                                                               Leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 3132)
                                                                                                                                                                                                                                                                                              Chem.
/codon_start=1
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pl10 delta;
/db_xref="pID:g2331238"
                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="spleen"
                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                  Chemistry,
Ann Arbor,
                                   3-kinase catalytic subunit
                                                                                                                                                                                    University of MI 48109-0636,
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tkqvimhraqyeblehtlsdebayvftcvnqyabqqbeledqrricdiqftlpvlrlv
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alernktuvqaklfhgnebalcktvsssevnvcsepvmkqrlebdisvcdlprakrich
altyavvekakkarstkkkskkadcpiamanlmlfdykdqlktgerclymmpsvpdekg
                                                    NWLAHNVSKDNRQ"
                                                                                   FLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEEALKHFRVKFNEALRESWKTKV
                                                                                                                                            LGNFKTKFGINRERVPFILTYDFVHVIQQGKTNNSEKFERFRGYCERAYTILRRHGLL
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δÃ Š В Qy 밁 밁 Š 밁 Š 밁 Q 밁 Š 밁 밁 В S Query Match Best Local Sin Matches 272; 3083 3404 3164 3104 3023 3344 2906 3284 2846 3224 2792 2732 2672 3044 AGGATCGTCACAGTGATAATCTGATGCTCACTGAAGATGGAAAATATGTCCACATTGATT 3103 2612 3464 CCAAAACGAATTGGCTCTTCCACGCAGT 3491 2966 2984 TCGATCGATTCCTATACTCGTGTGTTGGATATTCAGTTGCCACGTACATAATGGGAATCA 3043 CGACGAAAGCGGATTTGGATCATTTGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAG TCGGTCACATTTTGGGACACGGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCGT 3163 CCAAAGTCAACTGGCTGGCGCACAATGT AAGAGGCGCTAAAGCACTTCCGGGTGAAGTTCAACGAAGCTCTCCGAGAAAGCTGGAAAA AAGAAGCGAGAAAGTTTTTCGCTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCTA 3463 GCTGCTCCAAAGATATCCAGTATCTCAAGGACTCTC---TGGCACTGGGGAAGACGGAGG ACGGGCTGCTTTTCCTCCATCTCTTCGCCCTGATGCGGGCCGCAGGTCTGCCTGAGCTTA 2965 ATCGAGATTTGTTCGTTTCCTTGTTCACCTTGATGCTCGGAATGGAGTTGCCTGAGCTGT 3343 GTGAGAAGTTTGAAAGGTTCCGCGGCTACTGTGAACGAGCCTATACCATCCTGCGGCGCC 2905 CGCATGAGCTACAAAAATTCAAAACGTTATGCGTCGAAGCCTACGAAGTAATGTGGAATA 3283 TCATTCTCACCTACGACTTTGTCCACGTGATCCAGCAGGGGAA-----TTGGCCACTTTCTGGGGAACTTCAAGACCAAGTTTGGAATCAACCGAGAGCGCGTCCCCT GTGACCGGCACAGCGACAACATCATGATCAGAGAGAGGGGCAGCTCTTCCACATTGATT TTGAGGAATTCACCCTCTCCTGTGCTGGCTACTGTGTGGCCACATATGTTCTGGGCATCG 2671. Similarity Conservative 3.0%; 53.5%; Score 106.8; DE Pred. No. 4.8e-10; Mismatches 3110 DB 13; Be-17; 227; Indels Length -GACTAACAACA 2845 9; Gaps 3022 3082 3403 2731 2

RESULT 14 HSP110DEL

KEYWORDS ACCESSION DEFINITION Snoo

g2104839 p110delta; Homo sapiens

phosphoinositide 3-kinase

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H.sapiens Y10055

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bp RNA PRI
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3240 ATTCAAAACGTTATGCGTCGAAGCCTACGAAGTAATGTGGAATAATCGAGATTTGTTCGT 3299
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                                                                                                ACACGGAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCGTTTATTCTAACCGAACA 3179
                                                                                                                                                                                                                                                                                                CAACATCATGATCCGAGAGAGTGGGCAGCTGTTCCACATTGATTTTGGCCACTTTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTGTGCTGGCTATTGTGTGGCCACATATGTGCTGGGCATTGGCGATCGGCACAGCGA 2886
                                                          CTTTGTCCATGTGATTCAGCAGGGGAA-----GACTAATAATAGTGAGAAATTTGAACG 3060
                                                                                                                                                                             GAATTTCAAGACCAAGTTTGGAATCAACCGCGAGCGTGTCCCATTCATCCTCACCTACGA 3006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Street,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers
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ADERKKLVVQACLFHCNEMLCKTVSSSEVSVCSEPVMKQRLEFDINICDLFRMARLCF
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ALYAVIEKAKKARSTKKKSKADLPILAMRLMLFDYKQLKTEGRHSECVHVTEBEQ
ELLNPGGTVRSMPNTDSAAALLICLFBVAPHPVYYPALEKILELGRHSECVHVTEBEQ
LQLREILERRGSGLYEHEKDLVMKLRHEVQEHFPEALARLLLVTKMWKHEDVAQMLY
LLCSWPELPVLSALEILDFSFDCHVGSFAIKSLRKLTDDELFGLIPALLQVQVLKYESY
LLCSWPELPVLSALEILDFSFDCHVGSFAIKSLRKLTDDELFGLIPALLQVQVLKYESY
LDCELTKFLLDRALANRKIGHFLFWHLRSEMHYPSVALGHLPALGHLQSFDLPSTL
MKQGEALSKLKALNDEYKLSSQKTPKPQTKELMHCVARQEAYLEALSHLQSFDLPSTL
LAEVCVEQCTFMDSKMKPLMIMYSNEEBAGSGSVGIIFKNGDDLRQDMLTLQMIQLM
VLMKQBEGLDLRMTPYGCLPTGDRTGLLEVVLRSDTIANIQLMKSNMAATAAFNKDALL
VLMKQBEGLDLRMTPYGCLPTGDRTGLLEVVLRSDTIANIQLMKSNMAATAAFNKDALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"phosphoinositide 3-kinase"
/db_xref-"pid:e308053"
/db_xref-"pid:e308053"
/db_xref-"pid:e308053"
/db_xref-"pid:e308053"
/translation-"MPPGVDCPMEFWTKEENQSVVDDFLLPTGVYLNEFVSRNANLST
/KGLMHRAQVEPLFHMLSGPEAVYFTCINQTAEQQELEDEQRRICDVOPLFLYURLV
AREGDRYKKINSQ15LLIGKGLHEFDSLCDPEVNDFRAKMQGFCEEAAARRQQUFLALMA
AREGDRYKKINSQ15LLIGKGLHEFDSLCDPEVNDFRAKMQGFCEEAAARRQDVPLALMA
CALRKKATVFRQPLYEQPEDYTLQVNGRHEYLYGSYPLCQFQYICSCLHSGLTPHLTM
CALRKKATVFRQPLYEQPEDYTLQVNGRHEYLYGSYPLCQFQYICSCLHSGLTPHLTM
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1190 c 1141 g
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FLGNFKTKFGINRERVPFILTYDFVHVIQQGKTNNSEKFERFRGYCERAYTILRRHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEEALKHFRVKFNEALRESWKTF
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/db_xref="taxon:9606"
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1 (bases 1 to 5220)
Chantry,D., Vojtek,A., Kashishian,A., Holtzman,D.A., Wood,C., Gray,F.W., Cooper,J.A. and Hoekstra,M.F.
pliddelta, a novel phosphatidylinositol 3-kinase catalytic subunit that associates with p85 and is expressed predominantly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JAN-1997) Leukocyte Biochemistry, 22021 20th Ave. S.E., Bothell, WA 981021, USA
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LLCSWPELFYLSALELLDFSFPDCHYGSFAIKSLRKLTDDELFQYLLQLVQVLKYESY
LDCELTKFLLDRALANRKIGHFLFWHLRSEMHYPSVALRFGLILEAYCRGSTHHMKYL
MKQGEALSKLKALNDFYKLSSQKTPKPQTKELMHLCMRQEAYLEALSHLQSPLDPSTL
                                                                         AWLOYSFPLOLEPSAOTWGGGTLRLPNRALLVNVKFEGSESETFOVSTKDVPLALMA
CALRKKATVFROPLVEOPEDYTLQVNGRHEYLYDLORGYD ICSCLHSGLITHLITM
VHSSSILAMEDEGSNPAPOVOKPRAKPPPIPAKKPSSVSLWGLEOPFRIEBLIOGSKVN
VHSSSILAMEDEGSNPAPOVOKPRAKPPPIPAKKPSSVSLWGLEOPFRIEBLIOGSKVN
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                                                                                                                                                                                                                                                                                                                                                                  /product="phosphatidylinositol 3-kinase catalytic
pllodelta"
                                                                                                                                                                                                                                                              AREGDRVKKLINSQISLLIGKGLHEFDSLCDPEVNDFRAKMCQFCEEAAARRQQLGWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="PI-3 kinase catalytic subunit"
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Best Local Similarity 53.7%;
Matches 264; Conservative
                                                                                                                                                                                                                                                                              . 3120 CCACCTCTTTGCCCTGATGCGGGGGGGCAGGCCTGCCTGAGCTCAGCTGCTCCAAAGACAT 3179
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                                                                                                                                3420 TTTCGCTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCTACCAAAACGAATTGGCT 3479
                                                                                                                                                                                   3180 CCAGTATCTCAAGGACTCCC---TGGCACTGGGGAAAACAGAGGAGGAGGCACTGAAGCA 3236
                                                                                                                                                                                                                                 3360 GGATCATTTGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAAGAAGAAGAAGCGAGAAAGTT 3419
                                                                                                                                                                                                                                                                                                         3300 TTCCTTGTTCACCTTGATGCTCGGAATGGAGTTGCCTGAGCTGTCGACGAAAGCGGATTT 3359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2946 GAATTTCAAGACCAAGTTTGGAATCAACCGCGAGCGTGTCCCATTCATCCTCACCTATGA 3005
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3297 GGCCCACAACGT 3308
                                           3480 CTTCCACGCAGT 3491
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                                                                                           CTTCCGAGTGAAGTTTAACGAAGCCCTCCGTGAGAGCTGGAAAACCAAAGTGAACTGGCT 3296
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LFLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEEALKHFRVKFNEALRESWKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103.6; DB 11; Length 5220; Pred. No. 3.3e-16; O; Mismatches 219; Indels 9; Gaps
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